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(54) Title: HLA-BINDING PEPTIDES AND THEIR USES

(57) Abstract

The present invention provides the means and methods for selecting immunogenic peptides and the immunogenic peptide compositions capable of specifically binding glycoproteins encoded by HLA allele and inducing T cell activation in T cells restricted by the allele. The peptides are useful to elicit an immune response against a desired antigen.

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HLA BINDING PEPTIDES AND THEIR USES

BACKGROUND OF THE INVENTION

The present invention relates to compositions and methods for preventing, treating or diagnosing a number of pathological states such as viral diseases and cancers. In particular, it provides novel peptides capable of binding selected major histocompatibility complex (MHC) molecules and inducing an immune response.

MHC molecules are classified as either Class I or Class II molecules. Class II MHC molecules are expressed primarily on cells involved in initiating and sustaining immune responses, such as T lymphocytes, B lymphocytes, macrophages, etc. Class II MHC molecules are recognized by helper T lymphocytes and induce proliferation of helper T lymphocytes and amplification of the immune response to the particular immunogenic peptide that is displayed. Class I MHC molecules are expressed on almost all nucleated cells and are recognized by cytotoxic T lymphocytes (CTLs), which then destroy the antigen-bearing cells. CTLs are particularly important in tumor rejection and in fighting viral infections.

The CTL recognizes the antigen in the form of a peptide fragment bound to the MHC class I molecules rather than the intact foreign antigen itself. The antigen must normally be endogenously synthesized by the cell, and a portion of the protein antigen is degraded into small peptide fragments in the cytoplasm. Some of these small peptides translocate into a pre-Golgi compartment and interact with class I heavy chains to facilitate proper folding and association with the subunit β2 microglobulin. The peptide-MHC class I complex is then routed to the cell surface for expression and potential recognition by specific CTLs.

Investigations of the crystal structure of the human MHC class I molecule, HLA-A2.1, indicate that a peptide binding groove is created by the folding of the α1 and α2 domains of the class I heavy chain (Bjorkman et al., Nature 329:506 (1987). In these investigations, however, the identity of peptides bound to the groove was not determined.

Buus et al., Science 242:1065 (1988) first described a method for acid elution of bound peptides from MHC. Subsequently, Rammensee and his coworkers (Falk

et al., Nature 351:290 (1991) have developed an approach to characterize naturally processed peptides bound to class I molecules. Other investigators have successfully achieved direct amino acid sequencing of the more abundant peptides in various HPLC fractions by conventional automated sequencing of peptides eluted from class I molecules of the B type (Jardetzky, et al., Nature 353:326 (1991) and of the A2.1 type by mass spectrometry (Hunt, et al., Science 225:1261 (1992). A review of the characterization of naturally processed peptides in MHC Class I has been presented by Rötzschke and Falk (Rötzschke and Falk, Immunol. Today 12:447 (1991).

Sette et al., Proc. Natl. Acad. Sci. USA 86:3296 (1989) showed that MHC allele specific motifs could be used to predict MHC binding capacity. Schaeffer et al., Proc. Natl. Acad. Sci. USA 86:4649 (1989) showed that MHC binding was related to immunogenicity. Several authors (De Bruijn et al., Eur. J. Immunol., 21:2963-2970 (1991); Pamer et al., 991 Nature 353:852-955 (1991)) have provided preliminary evidence that class I binding motifs can be applied to the identification of potential immunogenic peptides in animal models. Class I motifs specific for a number of human alleles of a given class I isotype have yet to be described. It is desirable that the combined frequencies of these different alleles should be high enough to cover a large fraction or perhaps the majority of the human outbred population.

Despite the developments in the art, the prior art has yet to provide a useful human peptide-based vaccine or therapeutic agent based on this work. The present invention provides these and other advantages.

SUMMARY OF THE INVENTION

The present invention provides compositions comprising immunogenic peptides having binding motifs for HLA molecules. The immunogenic peptides, which bind to the appropriate MHC allele, comprise conserved residues at certain positions which allow the peptides to bind desired HLA molecules.

Epitopes on a number of immunogenic target proteins can be identified using the peptides of the invention. Examples of suitable antigens include prostate cancer specific antigen (PSA), hepatitis B core and surface antigens (HBVc, HBVs) hepatitis C antigens, Epstein-Barr virus antigens, human immunodeficiency type-1 virus (HIV1), Kaposi's sarcoma herpes virus (KSHV), human papilloma virus (HPV) antigens, Lassa

virus, mycobacterium tuberculosis (MT), p53, CEA, trypanosome surface antigen (TSA) and Her2/neu. The peptides are thus useful in pharmaceutical compositions for both therapeutic and diagnostic applications.

In particular, the invention provides compositions comprising an immunogenic peptide having an HLA binding motif, which immunogenic peptide is a peptide shown in Tables 3-14. Also provided are peptides comprising a conservative substitution of a residue in a peptide shown in Table 3-14. The immunogenic peptide of the invention can be further linked to a second oligopeptide. In some embodiments, the second oligopeptide is a peptide that induces a helper T response.

The invention further provides nucleic acid molecules encoding immunogenic peptides as shown in Tables 3-14, or peptides comprising a conservative substitution of a residue of a peptide shown in Table 3-14. The nucleic acid may further comprise a sequence encoding a second immunogenic peptide or peptide that induces a helper T response.

The peptides provided here can be used to induce a cytotoxic T cell response either *in vivo* or *in vitro*. The methods comprise contacting a cytotoxic T cell with a peptide of the invention.

Definitions

The term "peptide" is used interchangeably with "oligopeptide" in the present specification to designate a series of residues, typically L-amino acids, connected one to the other typically by peptide bonds between the alpha-amino and carbonyl groups of adjacent amino acids. The oligopeptides of the invention are less than about 15 residues in length and usually consist of between about 8 and about 11 residues, preferably 9 or 10 residues.

An "immunogenic peptide" is a peptide which comprises an allele-specific motif such that the peptide will bind an MHC molecule and induce a CTL response. Immunogenic peptides of the invention are capable of binding to an appropriate HLA molecule and inducing a cytotoxic T cell response against the antigen from which the immunogenic peptide is derived.

Immunogenic peptides are conveniently identified using the algorithms of the invention. The algorithms are mathematical procedures that produce a score which

enables the selection of immunogenic peptides. Typically one uses the algorithmic score with a "binding threshold" to enable selection of peptides that have a high probability of binding at a certain affinity and will in turn be immunogenic. The algorithm is based upon either the effects on MHC binding of a particular amino acid at a particular position of a peptide or the effects on binding of a particular substitution in a motif containing peptide.

A "conserved residue" is an amino acid which occurs in a significantly higher frequency than would be expected by random distribution at a particular position in a peptide. Typically a conserved residue is one where the MHC structure may provide a contact point with the immunogenic peptide. At least one to three or more, preferably two, conserved residues within a peptide of defined length defines a motif for an immunogenic peptide. These residues are typically in close contact with the peptide binding groove, with their side chains buried in specific pockets of the groove itself. Typically, an immunogenic peptide will comprise up to three conserved residues, more usually two conserved residues.

As used herein, "negative binding residues" are amino acids which if present at certain positions will result in a peptide being a nonbinder or poor binder and in turn fail to be immunogenic i.e. induce a CTL response.

The term "motif" refers to the pattern of residues in a peptide of defined length, usually about 8 to about 11 amino acids, which is recognized by a particular MHC allele. The peptide motifs are typically different for each human MHC allele and differ in the pattern of the highly conserved residues and negative residues.

The binding motif for an allele can be defined with increasing degrees of precision. In one case, all of the conserved residues are present in the correct positions in a peptide and there are no negative residues in positions 1,3 and/or 7.

The phrases "isolated" or "biologically pure" refer to material which is substantially or essentially free from components which normally accompany it as found in its native state. Thus, the peptides of this invention do not contain materials normally associated with their in situ environment, e.g., MHC I molecules on antigen presenting cells. Even where a protein has been isolated to a homogenous or dominant band, there are trace contaminants in the range of 5-10% of native protein which co-purify with the desired protein. Isolated peptides of this invention do not contain such endogenous co-purified protein.

The term "residue" refers to an amino acid or amino acid mimetic incorporated in an oligopeptide by an amide bond or amide bond mimetic.

DESCRIPTION OF THE PREFERRED EMBODIMENTS

The present invention relates to the determination of allele-specific peptide motifs for human Class I MHC (sometimes referred to as HLA) allele subtypes, in particular, peptide motifs recognized by HLA alleles.

For HLA-A2.1 alleles a peptide of 9 amino acids preferrably has the following motif: a first conserved residue at the second position from the N-terminus selected from the group consisting of I, V, A and T and a second conserved residue at the C-terminal position selected from the group consisting of V, L, I, A and M. An alternate motif is one in which the first conserved residue at the second position from the N-terminus selected is from the group consisting of L, M, I, V, A and T and the second conserved residue at the C-terminal position selected from the group consisting of A and M. The amino acid at position 1 is preferrably not an amino acid selected from the group consisting of D, and P. The amino acid at position 3 from the N-terminus is not an amino acid selected from the group consisting of D, E, R, K and H. The amino acid at position 6 from the N-terminus is not an amino acid selected from the group consisting of R, K and H. The amino acid at at position 7 from the N-terminus is not an amino acid selected from the group consisting of R, K, H, D and E.

The HLA-A2.1 binding motif for peptide of 10 residues is as follows: a first conserved residue at the second position from the N-terminus selected from the group consisting of L, M, I, V, A, and T, and a second conserved residue at the C-terminal position selected from the group consisting of V, I, L, A and M. The first and second conserved residues are separated by 7 residues. Preferrably, the amino acid at position 1 is not an amino acid selected from the group consisting of D, E and P. The N-terminal residue is not an amino acid selected from the group consisting of D and E. The residue at position 4 from the N-terminus is not an amino acid selected from the group consisting of A, K, R and H. The amino acid at positon 5 from the N-terminus is not P. The amino acid at position 7 from the N-terminus is not an amino acid selected from the group consisting of R, K and H. The amino acid at position 8 from the N-terminus is not amino acid selected from the group consisting of D, E, R, K and H. The amino acid at position

9 from the N-terminus is not an amino acid selected from the group consisting of R, K and H.

Te motif for HLA-A3.2 comprises from the N-terminus to C-terminus a first conserved residue of L, M, I, V, S, A, T and F at position 2 and a second conserved residue of K, R or Y at the C-terminal end. Other first conserved residues are C, G or D and alternatively E. Other second conserved residues are H or F. The first and second conserved residues are preferably separated by 6 to 7 residues.

The motif for HLA-A1 comprises from the N-terminus to the C-terminus a first conserved residue of T, S or M, a second conserved residue of D or E, and a third conserved residue of Y. Other second conserved residues are A, S or T. The first and second conserved residues are adjacent and are preferably separated from the third conserved residue by 6 to 7 residues. A second motif consists of a first conserved residue of E or D and a second conserved residue of Y where the first and second conserved residues are separated by 5 to 6 residues.

The motif for HLA-A11 comprises from the N-terminus to the C-terminus a first conserved residue of T, V, M, L, I, S, A, G, N, C D, or F at position 2 and a C-terminal conserved residue of K, R, Y or H. The first and second conserved residues are preferably separated by 6 or 7 residues.

The motif for HLA-A24.1 comprises from the N-terminus to the C-terminus a first conserved residue of Y, F or W at position 2 and a C terminal conserved residue of F, I, W, M or L. The first and second conserved residues are preferably separated by 6 to 7 residues.

These motifs are then used to define T cell epitopes from any desired antigen, particularly those associated with human viral diseases, cancers or autoiummune diseases, for which the amino acid sequence of the potential antigen or autoantigen targets is known.

Epitopes on a number of potential target proteins can be identified in this manner. Examples of suitable antigens include prostate specific antigen (PSA), hepatitis B core and surface antigens (HBVc, HBVs) hepatitis C antigens, Epstein-Barr virus antigens, melanoma antigens (e.g., MAGE-1), human immunodeficiency virus (HIV) antigens, human papilloma virus (HPV) antigens, Lassa virus, mycobacterium tuberculosis (MT), p53, CEA, trypanosome surface antigen (TSA) and Her2/neu.

Peptides comprising the epitopes from these antigens are synthesized and then tested for their ability to bind to the appropriate MHC molecules in assays using, for example, purified class I molecules and radioiodonated peptides and/or cells expressing empty class I molecules by, for instance, immunofluorescent staining and flow microfluorometry, peptide-dependent class I assembly assays, and inhibition of CTL recognition by peptide competition. Those peptides that bind to the class I molecule are further evaluated for their ability to serve as targets for CTLs derived from infected or immunized individuals, as well as for their capacity to induce primary in vitro or in vivo CTL responses that can give rise to CTL populations capable of reacting with virally infected target cells or tumor cells as potential therapeutic agents.

The MHC class I antigens are encoded by the HLA-A, B, and C loci. HLA-A and B antigens are expressed at the cell surface at approximately equal densities, whereas the expression of HLA-C is significantly lower (perhaps as much as 10-fold lower). Each of these loci have a number of alleles. The peptide binding motifs of the invention are relatively specific for each allelic subtype.

For peptide-based vaccines, the peptides of the present invention preferably comprise a motif recognized by an MHC I molecule having a wide distribution in the human population. Since the MHC alleles occur at different frequencies within different ethnic groups and races, the choice of target MHC allele may depend upon the target population. Table 1 shows the frequency of various alleles at the HLA-A locus products among different races. For instance, the majority of the Caucasoid population can be covered by peptides which bind to four HLA-A allele subtypes, specifically HLA-A2.1, A1, A3.2, and A24.1. Similarly, the majority of the Asian population is encompassed with the addition of peptides binding to a fifth allele HLA-A11.2.

TABLE 1

A Allele/Subtype	N(69)*	A(54)	C(502)
A1	10.1(7)	1.8(1)	27.4(138)
A2.1	11.5(8)	37.0(20)	39.8(199)
A2.2	10.1(7)	0	3.3(17)
A2.3	1.4(1)	5.5(3)	0.8(4)
A2.4	-	-	-
A2.5	-	-	-
A3.1	1.4(1)	0	0.2(0)
A3.2	5.7(4)	5.5(3)	21.5(108)
A11.1	0	5.5(3)	0
A11.2	5.7(4)	31.4(17)	8.7(44)
A11.3	0	3.7(2)	0
A23	4.3(3)	-	3.9(20)
A24	2.9(2)	27.7(15)	15.3(77)
A24.2	-	-	-
A24.3	-	-	-
A25	1.4(1)	-	6.9(35)
A26.1	4.3(3)	9.2(5)	5.9(30)
A26.2	7.2(5)	-	1.0(5)
A26V	-	3.7(2)	-
A28.1	10.1(7)	-	1.6(8)
A28.2	1.4(1)	-	7.5(38)
A29.1	1.4(1)	-	1.4(7)
A29.2	10.1(7)	1.8(1)	5.3(27)
A30.1	8.6(6)	-	4.9(25)
A30.2	1.4(1)	-	0.2(1)
A30.3	7.2(5)	-	3.9(20)
A31	4.3(3)	7.4(4)	6.9(35)
A32	2.8(2)	-	7.1(36)
Aw33.1	8.6(6)	-	2.5(13)
Aw33.2	2.8(2)	16.6(9)	1.2(6)
Aw34.1	1.4(1)	-	-
Aw34.2	14.5(10)	-	0.8(4)
Aw36	5.9(4)	-	-

Table compiled from B. DuPont, Immunobiology of HLA, Vol. I, Histocompatibility Testing 1987, Springer-Verlag, New York 1989.

* N - negroid; A = Asian; C = caucasoid. Numbers in parenthesis represent the number of individuals included in the analysis.

The nomenclature used to describe peptide compounds follows the conventional practice wherein the amino group is presented to the left (the N-terminus)

and the carboxyl group to the right (the C-terminus) of each amino acid residue. In the formulae representing selected specific embodiments of the present invention, the amino- and carboxyl-terminal groups, although not specifically shown, are in the form they would assume at physiologic pH values, unless otherwise specified. In the amino acid structure formulae, each residue is generally represented by standard three letter or single letter designations. The L-form of an amino acid residue is represented by a capital single letter or a capital first letter of a three-letter symbol, and the D-form for those amino acids having D-forms is represented by a lower case single letter or a lower case three letter symbol. Glycine has no asymmetric carbon atom and is simply referred to as "Gly" or G.

The procedures used to identify peptides of the present invention generally follow the methods disclosed in Falk et al., Nature 351:290 (1991), which is incorporated herein by reference. Briefly, the methods involve large-scale isolation of MHC class I molecules, typically by immunoprecipitation or affinity chromatography, from the appropriate cell or cell line. Examples of other methods for isolation of the desired MHC molecule equally well known to the artisan include ion exchange chromatography, lectin chromatography, size exclusion, high performance ligand chromatography, and a combination of all of the above techniques.

In the typical case, immunoprecipitation is used to isolate the desired allele. A number of protocols can be used, depending upon the specificity of the antibodies used. For example, allele-specific mAb reagents can be used for the affinity purification of the HLA-A, HLA-B_1, and HLA-C molecules. Several mAb reagents for the isolation of HLA-A molecules are available. The monoclonal BB7.2 is suitable for isolating HLA-A2 molecules. Affinity columns prepared with these mAbs using standard techniques are successfully used to purify the respective HLA-A allele products.

In addition to allele-specific mAbs, broadly reactive anti-HLA-A, B, C mAbs, such as W6/32 and B9.12.1, and one anti-HLA-B, C mAb, B1.23.2, could be used in alternative affinity purification protocols as described in previous applications.

The peptides bound to the peptide binding groove of the isolated MHC molecules are eluted typically using acid treatment. Peptides can also be dissociated from class I molecules by a variety of standard denaturing means, such as heat, pH, detergents, salts, chaotropic agents, or a combination thereof.

Peptide fractions are further separated from the MHC molecules by reversed-phase high performance liquid chromatography (HPLC) and sequenced. Peptides can be separated by a variety of other standard means well known to the artisan, including filtration, ultrafiltration, electrophoresis, size chromatography, precipitation with specific antibodies, ion exchange chromatography, isoelectrofocusing, and the like.

Sequencing of the isolated peptides can be performed according to standard techniques such as Edman degradation (Hunkapiller, M.W., et al., Methods Enzymol. 91, 399 [1983]). Other methods suitable for sequencing include mass spectrometry sequencing of individual peptides as previously described (Hunt, et al., Science 225:1261 (1992), which is incorporated herein by reference). Amino acid sequencing of bulk heterogenous peptides (e.g., pooled HPLC fractions) from different class I molecules typically reveals a characteristic sequence motif for each class I allele.

Definition of motifs specific for different class I alleles allows the identification of potential peptide epitopes from an antigenic protein whose amino acid sequence is known. Typically, identification of potential peptide epitopes is initially carried out using a computer to scan the amino acid sequence of a desired antigen for the presence of motifs. The epitopic sequences are then synthesized. The capacity to bind MHC Class molecules is measured in a variety of different ways. One means is a Class I molecule binding assay as described in the related applications, noted above. Other alternatives described in the literature include inhibition of antigen presentation (Sette, et al., J. Immunol. 141:3893 (1991), in vitro assembly assays (Townsend, et al., Cell 62:285 (1990), and FACS based assays using mutated ells, such as RMA.S (Melief, et al., Eur. J. Immunol. 21:2963 (1991)).

Next, peptides that test positive in the MHC class I binding assay are assayed for the ability of the peptides to induce specific CTL responses in vitro. For instance, Antigen-presenting cells that have been incubated with a peptide can be assayed for the ability to induce CTL responses in responder cell populations. Antigen-presenting cells can be normal cells such as peripheral blood mononuclear cells or dendritic cells (Inaba, et al., J. Exp. Med. 166:182 (1987); Boog, Eur. J. Immunol. 18:219 [1988]).

Alternatively, mutant mammalian cell lines that are deficient in their ability to load class I molecules with internally processed peptides, such as the mouse cell lines RMA-S (Kärre, et al.. Nature, 319:675 (1986); Ljunggren, et al., Eur. J. Immunol.

21:2963-2970 (1991)), and the human somatic T cell hybrid, T-2 (Cerundolo, et al., Nature 345:449-452 (1990)) and which have been transfected with the appropriate human class I genes are conveniently used, when peptide is added to them, to test for the capacity of the peptide to induce in vitro primary CTL responses. Other eukaryotic cell lines which could be used include various insect cell lines such as mosquito larvae (ATCC cell lines CCL 125, 126, 1660, 1591, 6585, 6586), silkworm (ATTC CRL 8851), armyworm (ATCC CRL 1711), moth (ATCC CCL 80) and Drosophila cell lines such as a Schneider cell line (see Schneider J. Embryol. Exp. Morphol. 27:353-365 [1927]).

Peripheral blood lymphocytes are conveniently isolated following simple venipuncture or leukapheresis of normal donors or patients and used as the responder cell sources of CTL precursors. In one embodiment, the appropriate antigen-presenting cells are incubated with 10-100 μM of peptide in serum-free media for 4 hours under appropriate culture conditions. The peptide-loaded antigen-presenting cells are then incubated with the responder cell populations in vitro for 7 to 10 days under optimized culture conditions. Positive CTL activation can be determined by assaying the cultures for the presence of CTLs that kill radiolabeled target cells, both specific peptide-pulsed targets as well as target cells expressing endogenously processed form of the relevant virus or tumor antigen from which the peptide sequence was derived.

Specificity and MHC restriction of the CTL is determined by testing against different peptide target cells expressing appropriate or inappropriate human MHC class I. The peptides that test positive in the MHC binding assays and give rise to specific CTL responses are referred to herein as immunogenic peptides.

The immunogenic peptides can be prepared synthetically, or by recombinant DNA technology or from natural sources such as whole viruses or tumors. Although the peptide will preferably be substantially free of other naturally occurring host cell proteins and fragments thereof, in some embodiments the peptides can be synthetically conjugated to native fragments or particles.

The polypeptides or peptides can be a variety of lengths, either in their neutral (uncharged) forms or in forms which are salts, and either free of modifications such as glycosylation, side chain oxidation, or phosphorylation or containing these modifications, subject to the condition that the modification not destroy the biological activity of the polypeptides as herein described.

Desirably, the peptide will be as small as possible while still maintaining substantially all of the biological activity of the large peptide. When possible, it may be desirable to optimize peptides of the invention to a length of 9 or 10 amino acid residues, commensurate in size with endogenously processed viral peptides or tumor cell peptides that are bound to MHC class I molecules on the cell surface.

Peptides having the desired activity may be modified as necessary to provide certain desired attributes, e.g., improved pharmacological characteristics, while increasing or at least retaining substantially all of the biological activity of the unmodified peptide to bind the desired MHC molecule and activate the appropriate T cell. For instance, the peptides may be subject to various changes, such as substitutions, either conservative or non-conservative, where such changes might provide for certain advantages in their use, such as improved MHC binding. By conservative substitutions is meant replacing an amino acid residue with another which is biologically and/or chemically similar, e.g., one hydrophobic residue for another, or one polar residue for another. The substitutions include combinations such as Gly, Ala; Val, Ile, Leu, Met; Asp, Glu; Asn, Gln; Ser, Thr; Lys, Arg; and Phe, Tyr. The effect of single amino acid substitutions may also be probed using D-amino acids. Such modifications may be made using well known peptide synthesis procedures, as described in e.g., Merrifield, Science 232:341-347 (1986), Barany and Merrifield, The Peptides, Gross and Meienhofer, eds. (N.Y., Academic Press), pp. 1-284 (1979); and Stewart and Young, Solid Phase Peptide Synthesis, (Rockford, Ill., Pierce), 2d Ed. (1984), incorporated by reference herein.

The peptides can also be modified by extending or decreasing the compound's amino acid sequence, e.g., by the addition or deletion of amino acids. The peptides or analogs of the invention can also be modified by altering the order or composition of certain residues, it being readily appreciated that certain amino acid residues essential for biological activity, e.g., those at critical contact sites or conserved residues, may generally not be altered without an adverse effect on biological activity. The non-critical amino acids need not be limited to those naturally occurring in proteins, such as L-α-amino acids, or their D-isomers, but may include non-natural amino acids as well, such as β-γ-δ-amino acids, as well as many derivatives of L-α-amino acids.

Typically, a series of peptides with single amino acid substitutions are employed to determine the effect of electrostatic charge, hydrophobicity, etc. on binding.

For instance, a series of positively charged (e.g., Lys or Arg) or negatively charged (e.g., Glu) amino acid substitutions are made along the length of the peptide revealing different patterns of sensitivity towards various MHC molecules and T cell receptors. In addition, multiple substitutions using small, relatively neutral moieties such as Ala, Gly, Pro, or similar residues may be employed. The substitutions may be homo-oligomers or hetero-oligomers. The number and types of residues which are substituted or added depend on the spacing necessary between essential contact points and certain functional attributes which are sought (e.g., hydrophobicity versus hydrophilicity). Increased binding affinity for an MHC molecule or T cell receptor may also be achieved by such substitutions, compared to the affinity of the parent peptide. In any event, such substitutions should employ amino acid residues or other molecular fragments chosen to avoid, for example, steric and charge interference which might disrupt binding.

Amino acid substitutions are typically of single residues. Substitutions, deletions, insertions or any combination thereof may be combined to arrive at a final peptide. Substitutional variants are those in which at least one residue of a peptide has been removed and a different residue inserted in its place. Such substitutions generally are made in accordance with the following Table 2 when it is desired to finely modulate the characteristics of the peptide.

TABLE 2

Original Residue	Exemplary Substitution
Ala	Ser
Arg	Lys, His
Asn	Gln
Asp	Glu
Cys	Ser
Gln	Asn
Glu	Asp
Gly	Pro
His	Lys; Arg
Ile	Leu; Val
Leu	Ile; Val
Lys	Arg; His
Met	Leu; Ile
Phe	Tyr; Trp
Ser	Thr
Thr	Ser
Trp	Tyr; Phe
Tyr	Trp; Phe
Val	Ile; Leu
Pro	Gly

Substantial changes in function (e.g., affinity for MHC molecules or T cell receptors) are made by selecting substitutions that are less conservative than those in Table 2, i.e., selecting residues that differ more significantly in their effect on maintaining (a) the structure of the peptide backbone in the area of the substitution, for example as a sheet or helical conformation, (b) the charge or hydrophobicity of the molecule at the target site or (c) the bulk of the side chain. The substitutions which in general are expected to produce the greatest changes in peptide properties will be those in which (a) hydrophilic residue, e.g. seryl, is substituted for (or by) a hydrophobic residue, e.g. leucyl, isoleucyl, phenylalanyl, valyl or alanyl; (b) a residue having an electropositive side chain, e.g., lysl, arginyl, or histidyl, is substituted for (or by) an electronegative residue, e.g. glutamyl or aspartyl; or (c) a residue having a bulky side chain, e.g. phenylalanine, is substituted for (or by) one not having a side chain, e.g., glycine.

The peptides may also comprise isosteres of two or more residues in the immunogenic peptide. An isostere as defined here is a sequence of two or more residues that can be substituted for a second sequence because the steric conformation of the first sequence fits a binding site specific for the second sequence. The term specifically includes peptide backbone modifications well known to those skilled in the art. Such modifications include modifications of the amide nitrogen, the α-carbon, amide carbonyl, complete replacement of the amide bond, extensions, deletions or backbone crosslinks. See, generally, Spatola, Chemistry and Biochemistry of Amino Acids, peptides and Proteins, Vol. VII (Weinstein ed., 1983).

Modifications of peptides with various amino acid mimetics or unnatural amino acids are particularly useful in increasing the stability of the peptide in vivo. Stability can be assayed in a number of ways. For instance, peptidases and various biological media, such as human plasma and serum, have been used to test stability. See, e.g., Verhoef et al., Eur. J. Drug Metab. Pharmacokin. 11:291-302 (1986). Half life of the peptides of the present invention is conveniently determined using a 25% human serum (v/v) assay. The protocol is generally as follows. Pooled human serum (Type AB, non-heat inactivated) is delipidated by centrifugation before use. The serum is then diluted to 25% with RPMI tissue culture media and used to test peptide stability. At predetermined time intervals a small amount of reaction solution is removed and added to either 6% aqueous trichloracetic acid or ethanol. The cloudy reaction sample is cooled

(4°C) for 15 minutes and then spun to pellet the precipitated serum proteins. The presence of the peptides is then determined by reversed-phase HPLC using stability-specific chromatography conditions.

The peptides of the present invention or analogs thereof which have CTL stimulating activity may be modified to provide desired attributes other than improved serum half life. For instance, the ability of the peptides to induce CTL activity can be enhanced by linkage to a sequence which contains at least one epitope that is capable of inducing a T helper cell response. Particularly preferred immunogenic peptides/T helper conjugates are linked by a spacer molecule. The spacer is typically comprised of relatively small, neutral molecules, such as amino acids or amino acid mimetics, which are substantially uncharged under physiological conditions. The spacers are typically selected from, e.g., Ala, Gly, or other neutral spacers of nonpolar amino acids or neutral polar amino acids. It will be understood that the optionally present spacer need not be comprised of the same residues and thus may be a hetero- or homo-oligomer. When present, the spacer will usually be at least one or two residues, more usually three to six residues. Alternatively, the CTL peptide may be linked to the T helper peptide without a spacer.

The immunogenic peptide may be linked to the T helper peptide either directly or via a spacer either at the amino or carboxy terminus of the CTL peptide. The amino terminus of either the immunogenic peptide or the T helper peptide may be acylated. Exemplary T helper peptides include tetanus toxoid 830-843, influenza 307-319, malaria circumsporozoite 382-398 and 378-389.

In some embodiments it may be desirable to include in the pharmaceutical compositions of the invention at least one component which primes CTL. Lipids have been identified as agents capable of priming CTL in vivo against viral antigens. For example, palmitic acid residues can be attached to the alpha and epsilon amino groups of a Lys residue and then linked, e.g., via one or more linking residues such as Gly, Gly-Gly-, Ser, Ser-Ser, or the like, to an immunogenic peptide. The lipidated peptide can then be injected directly in a micellar form, incorporated into a liposome or emulsified in an adjuvant, e.g., incomplete Freund's adjuvant. In a preferred embodiment a particularly effective immunogen comprises palmitic acid attached to alpha and epsilon amino groups

of Lys, which is attached via linkage, e.g., Ser-Ser, to the amino terminus of the immunogenic peptide.

As another example of lipid priming of CTL responses, E. coli lipoproteins, such as tripalmitoyl-S-glycerylcysteinlyseryl-serine (P_3CSS) can be used to prime virus specific CTL when covalently attached to an appropriate peptide. See, Deres et al., Nature 342:561-564 (1989), incorporated herein by reference. Peptides of the invention can be coupled to P_3CSS, for example, and the lipopeptide administered to an individual to specifically prime a CTL response to the target antigen. Further, as the induction of neutralizing antibodies can also be primed with P_3CSS conjugated to a peptide which displays an appropriate epitope, the two compositions can be combined to more effectively elicit both humoral and cell-mediated responses to infection.

In addition, additional amino acids can be added to the termini of a peptide to provide for ease of linking peptides one to another, for coupling to a carrier support, or larger peptide, for modifying the physical or chemical properties of the peptide or oligopeptide, or the like. Amino acids such as tyrosine, cysteine, lysine, glutamic or aspartic acid, or the like, can be introduced at the C- or N-terminus of the peptide or oligopeptide. Modification at the C terminus in some cases may alter binding characteristics of the peptide. In addition, the peptide or oligopeptide sequences can differ from the natural sequence by being modified by terminal-NH_2 acylation, e.g., by alkanoyl (C_1-C_{20}) or thioglycolyl acetylation, terminal-carboxyl amidation, e.g., ammonia, methylamine, etc. In some instances these modifications may provide sites for linking to a support or other molecule.

The peptides of the invention can be prepared in a wide variety of ways. Because of their relatively short size, the peptides can be synthesized in solution or on a solid support in accordance with conventional techniques. Various automatic synthesizers are commercially available and can be used in accordance with known protocols. See, for example, Stewart and Young, Solid Phase Peptide Synthesis, 2d. ed., Pierce Chemical Co. (1984), supra.

Alternatively, recombinant DNA technology may be employed wherein a nucleotide sequence which encodes an immunogenic peptide of interest is inserted into an expression vector, transformed or transfected into an appropriate host cell and cultivated under conditions suitable for expression. These procedures are generally known in the art,

as described generally in Sambrook et al., Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Press, Cold Spring Harbor, New York (1982), which is incorporated herein by reference. Thus, fusion proteins which comprise one or more peptide sequences of the invention can be used to present the appropriate T cell epitope.

As the coding sequence for peptides of the length contemplated herein can be synthesized by chemical techniques, for example, the phosphotriester method of Matteucci et al., J. Am. Chem. Soc. 103:3185 (1981), modification can be made simply by substituting the appropriate base(s) for those encoding the native peptide sequence. The coding sequence can then be provided with appropriate linkers and ligated into expression vectors commonly available in the art, and the vectors used to transform suitable hosts to produce the desired fusion protein. A number of such vectors and suitable host systems are now available. For expression of the fusion proteins, the coding sequence will be provided with operably linked start and stop codons, promoter and terminator regions and usually a replication system to provide an expression vector for expression in the desired cellular host. For example, promoter sequences compatible with bacterial hosts are provided in plasmids containing convenient restriction sites for insertion of the desired coding sequence. The resulting expression vectors are transformed into suitable bacterial hosts. Of course, yeast or mammalian cell hosts may also be used, employing suitable vectors and control sequences.

The peptides of the present invention and pharmaceutical and vaccine compositions thereof are useful for administration to mammals, particularly humans, to treat and/or prevent viral infection and cancer. Examples of diseases which can be treated using the immunogenic peptides of the invention include prostate cancer, hepatitis B, hepatitis C, AIDS, renal carcinoma, cervical carcinoma, lymphoma, CMV and condlyloma acuminatum.

For pharmaceutical compositions, the immunogenic peptides of the invention are administered to an individual already suffering from cancer or infected with the virus of interest. Those in the incubation phase or the acute phase of infection can be treated with the immunogenic peptides separately or in conjunction with other treatments, as appropriate. In therapeutic applications, compositions are administered to a patient in an amount sufficient to elicit an effective CTL response to the virus or tumor antigen and to cure or at least partially arrest symptoms and/or complications. An amount adequate to

accomplish this is defined as "therapeutically effective dose." Amounts effective for this use will depend on, e.g., the peptide composition, the manner of administration, the stage and severity of the disease being treated, the weight and general state of health of the patient, and the judgment of the prescribing physician, but generally range for the initial immunization (that is for therapeutic or prophylactic administration) from about 1.0 μg to about 5000 μg of peptide for a 70 kg patient, followed by boosting dosages of from about 1.0 μg to about 1000 μg of peptide pursuant to a boosting regimen over weeks to months depending upon the patient's response and condition by measuring specific CTL activity in the patient's blood. It must be kept in mind that the peptides and compositions of the present invention may generally be employed in serious disease states, that is, life-threatening or potentially life threatening situations. In such cases, in view of the minimization of extraneous substances and the relative nontoxic nature of the peptides, it is possible and may be felt desirable by the treating physician to administer substantial excesses of these peptide compositions.

For therapeutic use, administration should begin at the first sign of viral infection or the detection or surgical removal of tumors or shortly after diagnosis in the case of acute infection. This is followed by boosting doses until at least symptoms are substantially abated and for a period thereafter. In chronic infection, loading doses followed by boosting doses may be required.

Treatment of an infected individual with the compositions of the invention may hasten resolution of the infection in acutely infected individuals. For those individuals susceptible (or predisposed) to developing chronic infection the compositions are particularly useful in methods for preventing the evolution from acute to chronic infection. Where the susceptible individuals are identified prior to or during infection, for instance, as described herein, the composition can be targeted to them, minimizing need for administration to a larger population.

The peptide compositions can also be used for the treatment of chronic infection and to stimulate the immune system to eliminate virus-infected cells in carriers. It is important to provide an amount of immuno-potentiating peptide in a formulation and mode of administration sufficient to effectively stimulate a cytotoxic T cell response. Thus, for treatment of chronic infection, a representative dose is in the range of about 1.0 μg to about 5000 μg, preferably about 5 μg to 1000 μg for a 70 kg patient per dose.

Immunizing doses followed by boosting doses at established intervals, e.g., from one to four weeks, may be required, possibly for a prolonged period of time to effectively immunize an individual. In the case of chronic infection, administration should continue until at least clinical symptoms or laboratory tests indicate that the viral infection has been eliminated or substantially abated and for a period thereafter.

The pharmaceutical compositions for therapeutic treatment are intended for parenteral, topical, oral or local administration. Preferably, the pharmaceutical compositions are administered parenterally, e.g., intravenously, subcutaneously, intradermally, or intramuscularly. Thus, the invention provides compositions for parenteral administration which comprise a solution of the immunogenic peptides dissolved or suspended in an acceptable carrier, preferably an aqueous carrier. A variety of aqueous carriers may be used, e.g., water, buffered water, 0.8% saline, 0.3% glycine, hyaluronic acid and the like. These compositions may be sterilized by conventional, well known sterilization techniques, or may be sterile filtered. The resulting aqueous solutions may be packaged for use as is, or lyophilized, the lyophilized preparation being combined with a sterile solution prior to administration. The compositions may contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions, such as pH adjusting and buffering agents, tonicity adjusting agents, wetting agents and the like, for example, sodium acetate, sodium lactate, sodium chloride, potassium chloride, calcium chloride, sorbitan monolaurate, triethanolamine oleate, etc.

The concentration of CTL stimulatory peptides of the invention in the pharmaceutical formulations can vary widely, i.e., from less than about 0.1%, usually at or at least about 2% to as much as 20% to 50% or more by weight, and will be selected primarily by fluid volumes, viscosities, etc., in accordance with the particular mode of administration selected.

The peptides of the invention may also be administered via liposomes, which serve to target the peptides to a particular tissue, such as lymphoid tissue, or targeted selectively to infected cells, as well as increase the half-life of the peptide composition. Liposomes include emulsions, foams, micelles, insoluble monolayers, liquid crystals, phospholipid dispersions, lamellar layers and the like. In these preparations the peptide to be delivered is incorporated as part of a liposome, alone or in conjunction with a molecule which binds to, e.g., a receptor prevalent among lymphoid cells, such as monoclonal

antibodies which bind to the CD45 antigen, or with other therapeutic or immunogenic compositions. Thus, liposomes either filled or decorated with a desired peptide of the invention can be directed to the site of lymphoid cells, where the liposomes then deliver the selected therapeutic/immunogenic peptide compositions. Liposomes for use in the invention are formed from standard vesicle-forming lipids, which generally include neutral and negatively charged phospholipids and a sterol, such as cholesterol. The selection of lipids is generally guided by consideration of, e.g., liposome size, acid lability and stability of the liposomes in the blood stream. A variety of methods are available for preparing liposomes, as described in, e.g., Szoka et al., Ann. Rev. Biophys. Bioeng. 9:467 (1980), U.S. Patent Nos. 4,235,871, 4,501,728, 4,837,028, and 5,019,369, incorporated herein by reference.

For targeting to the immune cells, a ligand to be incorporated into the liposome can include, e.g., antibodies or fragments thereof specific for cell surface determinants of the desired immune system cells. A liposome suspension containing a peptide may be administered intravenously, locally, topically, etc. in a dose which varies according to, inter alia, the manner of administration, the peptide being delivered, and the stage of the disease being treated.

For solid compositions, conventional nontoxic solid carriers may be used which include, for example, pharmaceutical grades of mannitol, lactose, starch, magnesium stearate, sodium saccharin, talcum, cellulose, glucose, sucrose, magnesium carbonate, and the like. For oral administration, a pharmaceutically acceptable nontoxic composition is formed by incorporating any of the normally employed excipients, such as those carriers previously listed, and generally 10-95% of active ingredient, that is, one or more peptides of the invention, and more preferably at a concentration of 25%-75%.

For aerosol administration, the immunogenic peptides are preferably supplied in finely divided form along with a surfactant and propellant. Typical percentages of peptides are 0.01%-20% by weight, preferably 1%-10%. The surfactant must, of course, be nontoxic, and preferably soluble in the propellant. Representative of such agents are the esters or partial esters of fatty acids containing from 6 to 22 carbon atoms, such as caproic, octanoic, lauric, palmitic, stearic, linoleic, linolenic, olesteric and oleic acids with an aliphatic polyhydric alcohol or its cyclic anhydride. Mixed esters, such as mixed or natural glycerides may be employed. The surfactant may constitute 0.1%-20% by weight

of the composition, preferably 0.25-5%. The balance of the composition is ordinarily propellant. A carrier can also be included, as desired, as with, e.g., lecithin for intranasal delivery.

In another aspect the present invention is directed to vaccines which contain as an active ingredient an immunogenically effective amount of an immunogenic peptide as described herein. The peptide(s) may be introduced into a host, including humans, linked to its own carrier or as a homopolymer or heteropolymer of active peptide units. Such a polymer has the advantage of increased immunological reaction and, where different peptides are used to make up the polymer, the additional ability to induce antibodies and/or CTLs that react with different antigenic determinants of the virus or tumor cells. Useful carriers are well known in the art, and include, e.g., thyroglobulin, albumins such as human serum albumin, tetanus toxoid, polyamino acids such as poly(lysine:glutamic acid), influenza, hepatitis B virus core protein, hepatitis B virus recombinant vaccine and the like. The vaccines can also contain a physiologically tolerable (acceptable) diluent such as water, phosphate buffered saline, or saline, and further typically include an adjuvant. Adjuvants such as incomplete Freund's adjuvant, aluminum phosphate, aluminum hydroxide, or alum are materials well known in the art. And, as mentioned above, CTL responses can be primed by conjugating peptides of the invention to lipids, such as P_3CSS. Upon immunization with a peptide composition as described herein, via injection, aerosol, oral, transdermal or other route, the immune system of the host responds to the vaccine by producing large amounts of CTLs specific for the desired antigen, and the host becomes at least partially immune to later infection, or resistant to developing chronic infection.

Vaccine compositions containing the peptides of the invention are administered to a patient susceptible to or otherwise at risk of viral infection or cancer to elicit an immune response against the antigen and thus enhance the patient's own immune response capabilities. Such an amount is defined to be an "immunogenically effective dose." In this use, the precise amounts again depend on the patient's state of health and weight, the mode of administration, the nature of the formulation, etc., but generally range from about 1.0 μg to about 5000 μg per 70 kilogram patient, more commonly from about 10 μg to about 500 μg mg per 70 kg of body weight.

In some instances it may be desirable to combine the peptide vaccines of the invention with vaccines which induce neutralizing antibody responses to the virus of interest, particularly to viral envelope antigens.

For therapeutic or immunization purposes, nucleic acids encoding one or more of the peptides of the invention can also be admisitered to the patient. A number of methods are conveniently used to deliver the nucleic acids to the patient. For instance, the nulceic acid can be delivered directly, as "naked DNA". This approach is described, for instance, in Wolff *et. al.*, *Science* 247: 1465-1468 (1990) as well as U.S. Patent Nos. 5,580,859 and 5,589,466. The nucleic acids can also be administered using ballistic delivery as described, for instance, in U.S. Patent No. 5,204,253. Particles comprised solely of DNA can be administered. Alternatively, DNA can be adhered to particles, such as gold particles. The nucleci acids can also be delivered complexed to cationic compounds, such as cationic lipids. Lipid-mediated gene delivery methods are described, for instance, in WO 96/18372; WO 93/24640; Mannino and Gould-Fogerite (1988) *BioTechniques* 6(7): 682-691; Rose U.S. Pat No. 5,279,833; WO 91/06309; and Felgner *et al.* (1987) *Proc. Natl. Acad. Sci. USA* 84: 7413-7414. The peptides of the invention can also be expressed by attenuated viral hosts, such as vaccinia or fowlpox. This approach involves the use of vaccinia virus as a vector to express nucleotide sequences that encode the peptides of the invention. Upon introduction into an acutely or chronically infected host or into a noninfected host, the recombinant vaccinia virus expresses the immunogenic peptide, and thereby elicits a host CTL response. Vaccinia vectors and methods useful in immunization protocols are described in, e.g.,U.S. Patent No. 4,722,848, incorporated herein by reference. Another vector is BCG (Bacille Calmette Guerin). BCG vectors are described in Stover et al. (Nature 351:456-460 (1991)) which is incorporated herein by reference. A wide variety of other vectors useful for therapeutic administration or immunization of the peptides of the invention, e.g., Salmonella typhi vectors and the like, will be apparent to those skilled in the art from the description herein.

A preferred means of administering nucleic acids encoding the peptides of the invention uses minigene constructs encoding multiple epitopes of the invention. To create a DNA sequence encoding the selected CTL epitopes (minigene) for expression in human cells, the amino acid sequences of the epitopes are reverse translated. A human codon usage table is used to guide the codon choice for each amino acid. These epitope-encoding

DNA sequences are directly adjoined, creating a continuous polypeptide sequence. To optimize expression and/or immunogenicity, additional elements can be incorporated into the minigene design. Examples of amino acid sequence that could be reverse translated and included in the minigene sequence include: helper T lymphocyte epitopes, a leader (signal) sequence, and an endoplasmic reticulum retention signal. In addition, MHC presentation of CTL epitopes may be improved by including synthetic (e.g. poly-alanine) or naturally-occurring flanking sequences adjacent to the CTL epitopes.

The minigene sequence is converted to DNA by assembling oligonucleotides that encode the plus and minus strands of the minigene. Overlapping oligonucleotides (30-100 bases long) are synthesized, phosphorylated, purified and annealed under appropriate conditions using well known techniques. he ends of the oligonucleotides are joined using T4 DNA ligase. This synthetic minigene, encoding the CTL epitope polypeptide, can then cloned into a desired expression vector.

Standard regulatory sequences well known to those of skill in the art are included in the vector to ensure expression in the target cells. Several vector elements are required: a promoter with a down-stream cloning site for minigene insertion; a polyadenylation signal for efficient transcription termination; an *E. coli* origin of replication; and an *E. coli* selectable marker (e.g. ampicillin or kanamycin resistance). Numerous promoters can be used for this purpose, *e.g.*, the human cytomegalovirus (hCMV) promoter. *See*, U.S. Patent Nos. 5,580,859 and 5,589,466 for other suitable promoter sequences.

Additional vector modifications may be desired to optimize minigene expression and immunogenicity. In some cases, introns are required for efficient gene expression, and one or more synthetic or naturally-occurring introns could be incorporated into the transcribed region of the minigene. The inclusion of mRNA stabilization sequences can also be considered for increasing minigene expression. It has recently been proposed that immunostimulatory sequences (ISSs or CpGs) play a role in the immunogenicity of DNA vaccines. These sequences could be included in the vector, outside the minigene coding sequence, if found to enhance immunogenicity.

In some embodiments, a bicistronic expression vector, to allow production of the minigene-encoded epitopes and a second protein included to enhance or decrease immunogenicity can be used. Examples of proteins or polypeptides that could beneficially

enhance the immune response if co-expressed include cytokines (e.g., IL2, IL12, GM-CSF), cytokine-inducing molecules (e.g. LeIF) or costimulatory molecules. Helper (HTL) epitopes could be joined to intracellular targeting signals and expressed separately from the CTL epitopes. This would allow direction of the HTL epitopes to a cell compartment different than the CTL epitopes. If required, this could facilitate more efficient entry of HTL epitopes into the MHC class II pathway, thereby improving CTL induction. In contrast to CTL induction, specifically decreasing the immune response by co-expression of immunosuppressive molecules (e.g. TGF-β) may be beneficial in certain diseases.

Once an expression vector is selected, the minigene is cloned into the polylinker region downstream of the promoter. This plasmid is transformed into an appropriate *E. coli* strain, and DNA is prepared using standard techniques. The orientation and DNA sequence of the minigene, as well as all other elements included in the vector, are confirmed using restriction mapping and DNA sequence analysis. Bacterial cells harboring the correct plasmid can be stored as a master cell bank and a working cell bank.

Therapeutic quantities of plasmid DNA are produced by fermentation in *E. coli*, followed by purification. Aliquots from the working cell bank are used to inoculate fermentation medium (such as Terrific Broth), and grown to saturation in shaker flasks or a bioreactor according to well known techniques. Plasmid DNA can be purified using standard bioseparation technologies such as solid phase anion-exchange resins supplied by Quiagen. If required, supercoiled DNA can be isolated from the open circular and linear forms using gel electrophoresis or other methods.

Purified plasmid DNA can be prepared for injection using a variety of formulations. The simplest of these is reconstitution of lyophilized DNA in sterile phosphate-buffer saline (PBS). A variety of methods have been described, and new techniques may become available. As noted above, nucleic acids are conveniently formulated with cationic lipids. In addition, glycolipids, fusogenic liposomes, peptides and compounds referred to collectively as protective, interactive, non-condensing (PINC) could also be complexed to purified plasmid DNA to influence variables such as stability, intramuscular dispersion, or trafficking to specific organs or cell types.

Target cell sensitization can be used as a functional assay for expression and MHC class I presentation of minigene-encoded CTL epitopes. The plasmid DNA is

introduced into a mammalian cell line that is suitable as a target for standard CTL chromium release assays. The transfection method used will be dependent on the final formulation. Electroporation can be used for "naked" DNA, whereas cationic lipids allow direct *in vitro* transfection. A plasmid expressing green fluorescent protein (GFP) can be co-transfected to allow enrichment of transfected cells using fluorescence activated cell sorting (FACS). These cells are then chromium-51 labeled and used as target cells for epitope-specific CTL lines. Cytolysis, detected by 51Cr release, indicates production of MHC presentation of minigene-encoded CTL epitopes.

In vivo immunogenicity is a second approach for functional testing of minigene DNA formulations. Transgenic mice expressing appropriate human MHC molecules are immunized with the DNA product. The dose and route of administration are formulation dependent (e.g. IM for DNA in PBS, IP for lipid-complexed DNA). Twenty-one days after immunization, splenocytes are harvested and restimulated for 1 week in the presence of peptides encoding each epitope being tested. These effector cells (CTLs) are assayed for cytolysis of peptide-loaded, chromium-51 labeled target cells using standard techniques. Lysis of target cells sensitized by MHC loading of peptides corresponding to minigene-encoded epitopes demonstrates DNA vaccine function for *in vivo* induction of CTLs.

Antigenic peptides may be used to elicit CTL ex vivo, as well. The resulting CTL, can be used to treat chronic infections (viral or bacterial) or tumors in patients that do not respond to other conventional forms of therapy, or will not respond to a peptide vaccine approach of therapy. Ex vivo CTL responses to a particular pathogen (infectious agent or tumor antigen) are induced by incubating in tissue culture the patient's CTL precursor cells (CTLp) together with a source of antigen-presenting cells (APC) and the appropriate immunogenic peptide. After an appropriate incubation time (typically 1-4 weeks), in which the CTLp are activated and mature and expand into effector CTL, the cells are infused back into the patient, where they will destroy their specific target cell (an infected cell or a tumor cell).

The peptides may also find use as diagnostic reagents. For example, a peptide of the invention may be used to determine the susceptibility of a particular individual to a treatment regimen which employs the peptide or related peptides, and thus may be helpful in modifying an existing treatment protocol or in determining a prognosis for an affected

individual. In addition, the peptides may also be used to predict which individuals will be at substantial risk for developing chronic infection.

The following example is offered by way of illustration, not by way of limitation.

Example 1

Class I antigen isolation was carried out as described in the related applications, noted above. Naturally processed peptides were then isolated and sequenced as described there. An allele-specific motif and algorithms were determined and quantitative binding assays were carried out.

Using the motifs identified above for various HLA alleles, amino acid sequences from a number of antigens were analyzed for the presence of these motifs. Tables 3- ** provide the results of these searches.

The above examples are provided to illustrate the invention but not to limit its scope. Other variants of the invention will be readily apparent to one of ordinary skill in the art and are encompassed by the appended claims. All publications, patents, and patent applications cited herein are hereby incorporated by reference.

Table 3

Sequence	Antigen	Molecule
FTFSPTYKAFLSK	HBV	POL
GTLPQEHIVLKLK	HBV	POL
FTFSPTYKAFLCK	HBV	POL
GTLPQEHIVLKIK	HBV	POL
LVVSYVNTNMGLK	HBV	POL
STTDLEAYFKDCLFK	HBV	X
LVVSYVNVNMGLK	HBV	NUC
GTLPQDHIVQKIK	HBV	POL
STSSCLHQSAVRK	HBV	POL
TTVNAHQILPKVLHK	HBV	X
RTPARVTGGVFLVDK	HBV	POL

Sequence	Antigen	Molecule
HTTNFASK	HBV ayw	
FTFSPTYK	HBV ayw	
PTYKAFLCKQY	HBVayw	
CTTPAQGTSMY	HBVayw	
PTSCPPTCPGY	HBVayw	
FSQFSRGNY	HBVayw	
LMPLYACIQSK	HBVayw	
RVTGGVFLVDK	HBVayw	POL
HTLWKAGILYK	HBVayw	
QTRHYLHTLWK	HBVayw	
GTDNSVVLSRK	HBVayw	
SYVNTNMGLKF	HBVayw	
LYSILSPF	HBVayw	
WYWGPSLYSIL	HBVayw	
LYSILSPFLPL	HBVayw	
PYKEFGATVEL	HBVayw	
CTWMNSTGFTK	HCV	
MYVGDLCGSVF	HCV	
VYLLPRRGPRL	HCV	
ITKIQNFRVYY	HIV	
KVYLAWVPAHK	HIV	
KMIGGIGGFIK	HIV	
IVASCDKCQLK	HIV	
KVKQWPLTEEK	HIV	
TVNDIQKLVGK	HIV	
DVKQLTEAVQK	HIV	
AVVIQDNSDIK	HIV	
WTYQIYQEPFK	HIV	
VTVYYGVPVWK	HIV	
LTEDRWNKPQK	HIV	
ATDIQTKELQK	HIV	
QTKELQKQITK	HIV	

Sequence	Antigen	Molecule
WTVQPIVLPEK	HIV	
QVPLRPMTYK	HIV nef 73-82	
QVPLYPMTFK	HIV nef 73-82	
VPLRPMTYK	HIV nef 74-82	
AVDLYHFLK	HIV nef 84-94	
AVDLSHFLK	HIV nef 84-94	
ATLYCVHQR	HIV, p17, 82-90	
RLRDLLLIV	HIV-1 NL43 768-776	
RLRDLLLIVTR	HIV-1 NL43 768-778	
RLRDYLLIVTR	HIV-1 NL43 768-778	
LRDLLLIVTR	HIV-1 NL43 769-778	
QIYQEPFKNLK	HIV-1 RT 507-517	
AVFIHNFK	HIVcon	
RTLNAWVK	HIVcon	
ETAYFlLK	HIVcon	
RLRPGGKKK	HIVgag p17/2	
KIRLRPGGKK	HIVgag p17/2	
KIRLRPGGK	HIVgag p17/2	
ETTDLYCY	HPV16	E7
GTLGIVCPICSQK	HPV16	E7

Sequence	Antigen	Molecule
LMGTLGIVCPICSQK	HPV16	E7
AVCDKCLK	HPV16	E6
PYAVCDKCLKF	HPV16	E6
HYCYSLYGTTL	HPV16	E6
FYSRIREL	HPV16	E6
TLEKLTNTGLY	HPV18	E6
KTVLELTEVFEFAFK	HPV18	E6
TMLCMCCK	HPV18	E7
NTSLQDIEITCVYCK	HPV18	E6
EVFEFAFK	HPV18	E6
KQSSKALQR	Leukemia	þ3A2 CMI
ATGFKQSSK	Leukemia	þ3A2 CMI
HSATGFKQSSK	Leukemia	þ3A2 CMI
FKQSSKALQR	Leukemia	þ3A2 CMI
VTCLGLSY	MAGE1	
ITKKVADLVGFLLLK	MAGE1	
LVGFLLLK	MAGE1	
VTKAEMLESVIKNYK	MAGE1	
TSCILESLFR	MAGE1	
NYKHCFPEI	MAGE1	
SYVLVTCL	MAGE1	
ETDPISHTY	MAGE1(a)	
ETDPTSHLY	MAGE1(a)	
ETDPTSNTY	MAGE1(a)	
ETDPTSHVY	MAGE1(a)	
ETDPTSHSY	MAGE1(a)	
ETDPASHTY	MAGE1(a)	
EVDPTSHTY	MAGE1(a)	
ETDPTGHTY	MAGE1(a)	
ETDRTSHTY	MAGE1(a)	
EADPTSHTY	MAGE1(a)	
ETVPTSHTY	MAGE1(a)	

Sequence	Antigen	Molecule
ETDPTSHTY	MAGE1 consensus	
ETDPTGHSY	MAGE1 T(a)	
MFPDLESEF	MAGE2	
TTINYTLWR	MAGE2	
VIFSKASEY	MAGE2	
LVHFLLLKY	MAGE2	
LVHFLLLKY	MAGE2	
LVHFLLLKYR	MAGE2	
PVIFSKASEY	MAGE2	
STTINYTLWR	MAGE2	
VVEVVPISH	MAGE2	
EYLQLVFGI	MAGE2	
IFSKASEYL	MAGE2	
SFSTTINYTL	MAGE2	
LYILVTCLGL	MAGE2	
FATCLGLSY	MAGE3	
VVGNWQYFFPVIFSK	MAGE3	
LIIVLAIIAR	MAGE3	
YFFPVIFSK	MAGE3	
NWQYFFPVI	MAGE3	
NWQYFFPVIF	MAGE3	
IFSKASSSL	MAGE3	
EVDPTSNTY	MAGE41	
RYPLTFGWCY	nef/182	
RYPLTFGWC	nef/182	
ATQIPSYK	PAP	
LTELYFEK	PAP	
HSFPHPLY	PSA	
TQEPALGTTCY	PSA	
VTKFMLCAGRWTGGK	PSA	
HVISNDVCAQVHPQK	PSA	

Sequence	Antigen	Molecule
LYDMSLLKNRF	PSA	
ETDPTGHSY	T2 analog of MAGE-3	

Table 4

Peptide	Sequence	AA	Virus	Strain	Molecule	Pos.	Motif	A1	A2.1	A3.2	A11	A24
1.0300	IILDMLRHLY	9	c-ERB2			42	1	9.1		0.037	0.0012	
1.0346	LLDIDETEY	9	c-ERB2			869	1	7.6		0.0003	0	
1.0305	GTQLFEDNY	9	c-ERB2			104	1	0.18		0	0.028	
1.0355	LTCSPQPEY	9	c-ERB2			1131	1	0.13		0	0.0061	
1.0317	ETLEEITGY	9	c-ERB2			401	1	0.043		<0.0002	<0.0002	
1.0338	QLVTQLMPY	9	c-ERB2			795	1	0.0024		0.011	0.0039	
1.0749	FTHQSDVWSY	10	c-ERB2			899	1	2.7		0.0003	0.0005	
1.0747	RLLDIDETEY	10	c-ERB2			868	1	1.3		0.0017	0	
1.0715	TLEEITGYLY	10	c-ERB2			402	1	1.1		0	0	
1.0737	YVMAGVGSPY	10	c-ERB2			772	1	1.1	0	0.010	0.012	0
1.0764	GTPTAENPEY	10	c-ERB2			1239	1	0.063		<0.0002	0.0022	
1.0724	RVLQGLPREY	10	c-ERB2			545	1	<0.0015		0.035	0.0050	
1.0705	LIQRNPQLCY	10	c-ERB2			154	1	0.030		0.0012	<0.0002	
1.0693	VVQGNLELTY	10	c-ERB2			55	1	0.018		0.0024	0.011	
1.0756	MGDLVDAEEY	10	c-ERB2			1014	1	0.012		<0.0002	<0.0002	
1.1028	KIRKYTMRR	9	c-ERB2			681	3,11			0.76	0.0018	
1.1027	VVFGILIKR	9	c-ERB2			669	3,11			0.11	0.72	
1.0344	LVKSPNHVK	9	c-ERB2			852	3,11			0.48	0.070	
1.0335	VLRENTSPK	9	c-ERB2			754	3,11			0.40	0.013	
1.0329	ILIKRRQQK	9	c-ERB2			673	3,11			0.38	0.0097	
1.0311	ILWKDIFHK	9	c-ERB2			167	3,11			0.28	0.31	
1.1033	KITDFGLAR	9	c-ERB2			860	3,11			0.17	0.24	
1.0869	GVVFGILIK	9	c-ERB2			668	3,11			0.0047	0.089	
1.0299	QVCTGTDMK	9	c-ERB2			24	3,11			0.0007	0.052	
1.1031	LLDHVRENR	9	c-ERB2			806	3,11			0.037	<0.0006	
1.1026	CVNCSQFLR	9	c-ERB2			528	3,11			0.0015	0.031	
1.1023	TVCAGGCAR	9	c-ERB2			218	3,11			0.0004	0.023	
1.0331	ILKETELRK	9	c-ERB2			714	3,11			0.019	0.0023	
1.1024	VTAEDGTQR	9	c-ERB2			322	3,11			<0.0002	0.014	
1.0326	DLSYMPIWK	9	c-ERB2			607	3,11			0.0005	0.010	
1.0707	TILWKDIFHK	10	c-ERB2			166	3,11			0.043	3.6	
1.0712	GTQRCEKCSK	10	c-ERB2			327	3,11			0.021	0.61	
1.0736	KVLRENTSPK	10	c-ERB2			753	3,11			0.38	0.22	
1.0702	QLRSLTEILK	10	c-ERB2			141	3,11			0.20	0.013	
1.1142	RLVHRDLAAR	10	c-ERB2			840	3,11			0.18	0	
1.0741	LLNWCMQIAK	10	c-ERB2			822	3,11			0.14	0.14	
1.0752	TIDVYMIMVK	10	c-ERB2			948	3,11			0.013	0.12	

Peptide	Sequence	AA	Virus	Strain	Molecule	Pos.	Motif	A1	A2.1	A3.2	A11	A24
1.0731	RILKETELRK	10	c-ERB2			713	3,11			0.057	0.11	
1.0745	VLVKSPNHVK	10	c-ERB2			851	3,11			0.082	0.0072	
1.1131	SVFQNLQVIR	10	c-ERB2			423	3,11			0.017	0.075	
1.1133	HTVPWDQLFR	10	c-ERB2			478	3,11			0.0035	0.072	
1.1127	ILKGGVLIQR	10	c-ERB2			148	3,11			0.040	0.0005	
1.1143	LVSEFSRMAR	10	c-ERB2			972	3,11			0.0072	0.033	
1.1136	GVVFGILIKR	10	c-ERB2			668	3,11			0.018	0.033	
1.0726	CVARCPSGVK	10	c-ERB2			596	3,11			0.022	0.0042	
1.1137	VVFGILIKRR	10	c-ERB2			669	3,11			0.0030	0.016	
1.0728	GILIKRRQQK	10	c-ERB2			672	3,11			0.015	0.0014	
1.1129	RTVCAGGCAR	10	c-ERB2			217	3,11			0.0068	0.013	
1.1134	GLACHQLCAR	10	c-ERB2			508	3,11			0.011	0	
1.1139	KIPVAIKVLR	10	c-ERB2			747	3,11			0.0009	0.0099	

Peptide	Sequence	AA	Virus	Strain	Molecule	Pos.	Motif	A1	A2.1	A3.2	A11	A24
1.0291	VGEADYFEY	9	EBNA1			409	1	0.016				
1.0295	PLRESIVCY	9	EBNA1			553	1	0.010				
1.0681	PVGEADYFEY	10	EBNA1			408	1	0.015				
1.0683	GTWVAGVFVY	10	EBNA1			501	1	0.014				
1.0293	GVFVYGGSK	9	EBNA1			506	3,11			0.30	0.61	
1.1016	KTSLYNLRR	9	EBNA1			514	3,11			0.31	0.12	
1.0297	AIKDLVMTK	9	EBNA1			578	3,11			0.048	0.034	
1.0687	QTHIFAEVLK	10	EBNA1			567	3,11			0.010	0.21	
1.1124	GTALAIPQCR	10	EBNA1			523	3,11			0.0028	0.056	

Peptide	Sequence	AA	Virus	Strain	Molecule	Pos.	Motif	A1	A2.1	A3.2	A11	A24
5.0005	CTELKLSDY	9	FLU	A	NP	44	1	3.6				
5.0006	STLELRSRY	9	FLU	A	NP	377	1	0.020				
5.0044	ILRGSVAHK	9	FLU	A	NP	265	3			1.5	0.0037	
5.0051	RMCNILKGK	9	FLU	A	NP	221	3			0.27	0.062	
5.0046	LMQGSTLPR	9	FLU	A	NP	166	3			0.031	0.10	
5.0048	MIDGIGRFY	9	FLU	A	NP	32	3			0.059	0.0010	
5.0049	MVLSAFDER	9	FLU	A	NP	66	3			0.0016	0.041	
5.0054	YIQMCTELK	9	FLU	A	NP	40	3			0.0031	0.030	
5.0042	GINDRNFWR	9	FLU	A	NP	200	3			0.0028	0.024	
5.0104	SLMQGSTLPR	10	FLU	A	NP	165	3			0.12	0.84	
5.0095	KMIDGIGRFY	10	FLU	A	NP	31	3			0.50	0.0079	
5.0096	LILRGSVAHK	10	FLU	A	NP	264	3			0.36	0.037	
5.0102	RSGAAGAAVK	10	FLU	A	NP	175	3			0.019	0.0046	
5.0105	SSTLELRSRY	10	FLU	A	NP	376	3			0.0018	0.016	
5.0103	RSRYWAIRTR	10	FLU	A	NP	382	3			0.012	0	
5.0101	RMVLSAFDER	10	FLU	A	NP	65	3			0.0014	0.010	
5.0061	FYIQMCTEL	9	FLU	A	NP	39	24					2.9
5.0060	AYERMCNIL	9	FLU	A	NP	218	24					0.031
5.0112	RFYIQMCTEL	10	FLU	A	NP	38	24					0.15

Peptide	Sequence	AA	Virus	Strain	Molecule	Pos.	Motif	A1	A2.1	A3.2	A11	A24
1.0155	LLDTASALY	9	HBV	adr	CORE	420	1	25		0.0007	0	
1.0186	SLDVSAAFY	9	HBV	adr	POL	1001	1	17.2		0.0037	0.0006	
2.0125	PTTGRTSLY	9	HBV	ALL		1,382	1	1.3		0.0008	0	
2.0126	MSTTDLEAY	9	HBV	adr		1,521	1	0.85		<0.0008	0	
1.0208	PTTGRTSLY	9	HBV	adr	POL	1382	1	0.77		0	0	
1.0387	LTKQYLNLY	9	HBV	adw	POL	1280	1	0.50		0.0003	0.0075	
1.0166	KVGNFTGLY	9	HBV	adr	POL	629	1	0.068		0.30	0.014	
2.0127	MSPTDLEAY	9	HBV	adw		1,550	1	0.067				
2.0120	PSQPSRGNY	9	HBV	ayw		984	1	0.057				
2.0112	PSSWAFAKY	9	HBV	adw		316	1	0.054				
2.0119	QSAVRKEAY	9	HBV	adw		881	1	0.025				
1.0174	PLDKGIKPY	9	HBV	adr	POL	698	1	0.019		<0.0002	<0.0002	
1.0378	SLMLLYKTY	9	HBV	adw	POL	1092	1	0.017				
2.0115	ASRDLVVSY	9	HBV	ayw		499	1	0.013				
2.0124	PSRGRLGLY	9	HBV	adr/adw		1,364	1	0.011				
2.0121	SSTSRNINY	9	HBV	adr		1,036	1	0.0097				
1.0519	DLLDTASALY	10	HBV	adr	CORE	419	1	11.1		0	0	
1.0513	LLDPRVRGLY	10	HBV	adr	ENV	120	1	6.3		0.17	0	
2.0239	LSLDVSAAFY	10	HBV	ALL		1,000	1	4.2		<0.0009	0.0037	
1.0911	FLCQQYLHLY	10	HBV	adr	POL	1250	1	1.1	0.0025	0.014	0.0048	0.0017
2.0216	QTFGRKLHLY	10	HBV	ayw	POL	1087	1	1.1		0.0056	0.012	
2.0244	KTYGRKLHLY	10	HBV	adw		1,098	1	0.69	0.0003	0.59	0.22	0
1.0791	KTYGRKLHLY	10	HBV	adw	POL	1098	1	0.57	0.0020	0.53	0.35	0.0001
2.0242	QTFGRKLHLY	10	HBV	ayw		1,087	1	0.37		0.0037	0.011	
1.0556	KTFGRKLHLY	10	HBV	adr	POL	1069	1	0.34	0.0023	0.094	0.090	0
2.0241	KTFGRKLHLY	10	HBV	adr		1,069	1	0.30	0.0002	0.15	0.095	0
1.0766	LQDPRVRALY	10	HBV	adw	ENV	120	1	0.21		0.014	0	
1.0806	TTPAQGTSMY	10	HBV	adw	ENV	288	1	0.20		0	0	
2.0240	LSSTSRNINY	10	HBV	adr		1,035	1	0.20		<0.0009	0	
1.0541	PLDKGIKPYY	10	HBV	adr	POL	698	1	0.16		0	0	
2.0238	HSASFCGSPY	10	HBV	ayw		767	1	0.15	0	0.019	0.017	0
1.0795	FLTKQYLNLY	10	HBV	adw	POL	1279	1	0.12		0	0	
2.0237	RSASFCGSPY	10	HBV	adr/adw		738	1	0.11	0	0.033	0.020	0
1.0774	WLWGMDIDPY	10	HBV	adw	CORE	416	1	0.081		<0.0002	<0.0002	
2.0233	TTPAQGTSMY	10	HBV	ayw		288	1	0.066				
1.0542	HTLWKAGILY	10	HBV	adr	POL	723	1	0.030				
2.0231	TSCPPICPGY	10	HBV	adr		226	1	0.018				

Peptide	Sequence	AA	Virus	Strain	Molecule	Pos.	Motif	A1	A2.1	A3.2	A11	A24
2.0246	KSVQHLESLY	10	HBV	adw		1,161	1	0.016				
1.0910	NLYVSLLLLY	10	HBV	adr	POL	1059	1	0.015				
2.0089	LLYQTFGRK	9	HBV	ayw	POL	1084	3			1.8	0.64	
2.0116	IMPARFYPK	9	HBV	ayw		713	3			0.99	1.5	
2.0082	CLHQSPVRK	9	HBV	ayw	POL	867	3			0.14	0.025	
5.0056	SAICSVVRR	9	HBV		POL	531	3			<0.0003	0.067	
2.0077	HLHQDIIKK	9	HBV	ayw	POL	686	3			0.041	0.0075	
2.0219	SLPQEHIIQK	10	HBV	ayw	POL	1197	3			0.36	4.2	
2.0234	SMFPSCCCTK	10	HBV	adr/adw		295	3			0.43	1.9	
2.0235	SMYPSCCCTK	10	HBV	ayw		295	3			1.1	1.79	
5.0107	QAFTFSPTYK	10	HBV		POL	665	3			0.15	1.3	
2.0214	LLLYQTFGRK	10	HBV	ayw	POL	1083	3			0.89	0.021	
2.0245	YMDDVVLGAK	10	HBV	ALL		1,123	3			0.16	0.0076	
5.0108	TSAICSVVRR	10	HBV		POL	530	3			0.0006	0.013	
2.0094	PTYKAFLCK	9	HBV	ayw	POL	1263	11			0.030	0.085	
2.0068	PTDLEAYFK	9	HBV	adw	"X"	1552	11			0.0002	0.016	
2.0061	KYTSFPWLL	9	HBV	ALL		1,330	24					3.6
2.0059	LYAAVTNFL	9	HBV	adw		1,169	24					3.2
2.0046	FYPNLTKYL	9	HBV	adr		689	24					2.1
2.0045	LYSSTVPSF	9	HBV	adw/ayw		665	24					1.9
2.0048	FYPKVTKYL	9	HBV	ayw		718	24					1.7
2.0049	FYPNVTKYL	9	HBV	adw		718	24					1.6
2.0039	LYSILSPFL	9	HBV	ayw		368	24					0.50
2.0044	LYSSTVPVL	9	HBV	adr		636	24					0.37
2.0038	LYNILSPFL	9	HBV	adr		368	24					0.34
2.0051	NYRVSWPKF	9	HBV	ayw		991	24					0.18
2.0050	HYFQTRHYL	9	HBV	adw/ayw		743	24					0.15
2.0047	HYFKTRHYL	9	HBV	adr		714	24					0.057
2.0060	GYPALMPLY	9	HBV	ALL		1,224	24					0.049
5.0062	AYRPPNAPI	9	HBV		NUC;XNUCFUS	131	24					0.026
2.0054	LYQTFGRKL	9	HBV	ayw		1,085	24					0.014
2.0043	SYQHFRRLL	9	HBV	ayw		607	24					0.011
2.0181	LYSHPIILGF	10	HBV	ALL		1,077	24					1.1
2.0182	LYAAVTNFLL	10	HBV	adw		1,169	24					0.32
2.0188	LYRPLLSLPF	10	HBV	adr		1,371	24					0.25
2.0174	SYQHFRRLLL	10	HBV	ayw		607	24					0.16
2.0173	SYQHFRKLLL	10	HBV	adr/adw		578	24					0.066

Peptide	Sequence	AA	Virus	Strain	Molecule	Pos.	Motif	A1	A2.1	A3.2	A11	A24
2.0176	YYPEHLVNHY	10	HBV	ayw		735	24					0.040
2.0172	AYRPPNAPIL	10	HBV	ALL		521	24					0.022
2.0171	GYRWMCLRRF	10	HBV	ALL		234	24					0.011
5.0115	NFLLSLGIHL	10	HBV		POL	572	24					0.0099
1.0377	YVSLMLLYK	9	HBV	adw	POL	1090	3,11			0.31	7.4	
1.0189	LLYKTFGRK	9	HBV	adr	POL	1066	3,11			5.0	0.30	
1.0379	LLYKTYGRK	9	HBV	adw	POL	1095	3,11			2.5	0.40	
1.0370	VTKYLPLDK	9	HBV	adw	POL	722	3,11			0.014	1.3	
1.0176	RHYLHTLWK	9	HBV	adr	POL	719	3,11			1.2	0.010	
1.0367	STVPSFNPK	9	HBV	adw	POL	668	3,11			0.021	0.93	
1.0215	TTDLEAYFK	9	HBV	adr	"X"	1523	3,11			0.0006	0.92	
1.0848	YVSLLLLYK	9	HBV	adr	POL	1061	3,11			0.39	0.92	
1.0383	PTYKAFLTK	9	HBV	adw	POL	1274	3,11			0.17	0.71	
1.0987	HLYPVARQR	9	HBV	adr	POL	1257	3,11			0.54	0.0020	
1.0358	STNRQLGRK	9	HBV	adw	ENV	85	3,11			0.51	0.34	
1.0991	ALRFTSARR	9	HBV	adr	"X"	1488	3,11			0.44	<0.0005	
1.0197	PVNRPIDWK	9	HBV	adr	POL	1197	3,11			0.080	0.41	
1.0369	TVNENRRLK	9	HBV	adw	POL	703	3,11			0.016	0.40	
1.1041	VVNHYFQTR	9	HBV	adw	POL	740	3,11			0.030	0.33	
1.0152	STTSTGPCK	9	HBV	adr	ENV	277	3,11			0.011	0.29	
1.0213	QVLPKLLHK	9	HBV	adr	"X"	1505	3,11			0.10	0.28	
1.0172	LTKYLPLDK	9	HBV	adr	POL	693	3,11			0.0039	0.23	
1.0374	CLHQSAVRK	9	HBV	adw	POL	878	3,11			0.22	0.017	
1.0980	VVDFSQFSR	9	HBV	adr	POL	963	3,11			0.011	0.20	
1.0382	PLYACIQAK	9	HBV	adw	POL	1259	3,11			0.18	0.034	
2.0074	YVNTNMGLK	9	HBV	ayw	CORE	507	3,11			0.16	0.048	
1.0199	PLYACIQSK	9	HBV	adr	POL	1230	3,11			0.11	0.018	
1.0972	RLADEGLNR	9	HBV	adr	POL	601	3,11			0.10	0.025	
1.0976	AVNHYFKTR	9	HBV	adr	POL	711	3,11			0.0071	0.098	
1.0975	RLKLIMPAR	9	HBV	adr	POL	680	3,11			0.095	0.0002	
1.0977	ILYKRETTR	9	HBV	adr	POL	730	3,11			0.095	<0.0005	
1.0993	KVFVLGGCR	9	HBV	adr	"X"	1548	3,11			0.042	0.082	
1.0165	NVSIPWTHK	9	HBV	adr	POL	621	3,11			0.072	0.076	
1.0982	LLLYKTFGR	9	HBV	adr	POL	1065	3,11			0.072	0.0045	
1.0978	RLVFQTSTR	9	HBV	adr	POL	757	3,11			0.068	0.0032	
1.0219	FVLGGCRHK	9	HBV	adr	"X"	1550	3,11			0.065	0.019	
1.1042	RLVLQTSTR	9	HBV	adw	POL	786	3,11			0.064	0.0002	

Peptide	Sequence	AA	Virus	Strain	Molecule	Pos.	Motif	A1	A2.1	A3.2	A11	A24
1.1043	MLLYKTYGR	9	HBV	adw	POL	1094	3,11			0.061	0.0032	
1.0170	TVNEKRRLK	9	HBV	adr	POL	674	3,11			0.048	0.037	
1.1045	NLYPVARQR	9	HBV	adw	POL	1286	3,11			0.042	0.0011	
1.1046	LPYRPTTGR	9	HBV	adw	POL	1407	3,11			0.021	0	
1.0845	LVSFGVWIR	9	HBV	adr	CORE	509	3,11			0.0033	0.020	
1.0981	LVGSSGLPR	9	HBV	adr	POL	1022	3,11			0.0008	0.015	
1.0967	HISCLTFGR	9	HBV	adr	CORE	494	3,11			0.013	0.011	
1.1047	SVPSRLPDR	9	HBV	adw	POL	1424	3,11			0.0007	0.010	
1.0989	SVPSHLPDR	9	HBV	adr	POL	1395	3,11			0.0004	0.010	
1.0564	TLPQEHIVLK	10	HBV	adr	POL	1179	3,11			0.092	5.6	
2.0205	TVPVFNPHWK	10	HBV	ayw	POL	669	3,11			0.0067	4.2	
1.0543	TLWKAGILYK	10	HBV	adr	POL	724	3,11			3.5	1.0	
1.0807	SMYPSCCCTK	10	HBV	ayw	ENV	295	3,11			1.5	3.4	
1.1153	RLPYRPTTGR	10	HBV	adw	POL	1406	3,11			2.8	0.030	
1.0584	STTDLEAYFK	10	HBV	adr	'X'	1522	3,11			0.0066	2.7	
1.0554	LLLYKTFGRK	10	HBV	adr	POL	1065	3,11			2.5	0.012	
1.0799	TVNAHRNLPK	10	HBV	adw	"X"	1529	3,11			0.82	0.65	
1.0586	EAYFKDCLFK	10	HBV	adr	'X'	1527	3,11			0.037	0.74	
1.1081	LVVDFSQFSR	10	HBV	adr	POL	962	3,11			0.0009	0.63	
1.0789	MLLYKTYGRK	10	HBV	adw	POL	1094	3,11			0.61	0.020	
1.0546	TAYSHLSTSK	10	HBV	adr	POL	858	3,11			0.26	0.092	
1.0562	SLGIHLNPNK	10	HBV	adr	POL	1150	3,11			0.20	0.078	
1.1152	RLGLYRPLLR	10	HBV	adw	POL	1397	3,11			0.19	0.0049	
1.0547	VTGGVFLVDK	10	HBV	adr	POL	943	3,11			0.035	0.17	
1.1150	RIRTPRTPAR	10	HBV	adw	POL	962	3,11			0.17	0.0002	
1.0581	TVNGHQVLPK	10	HBV	adr	'X'	1500	3,11			0.073	0.092	
1.1091	SLPFQPTTGR	10	HBV	adr	POL	1377	3,11			0.077	0.043	
1.1072	TLPETTVVRR	10	HBV	adr	CORE	532	3,11			<0.0003	0.075	
1.1089	GTDNSVVLSR	10	HBV	adr	POL	1320	3,11			0.025	0.072	
1.1071	STLPETTVVR	10	HBV	adr	CORE	531	3,11			0.0005	0.068	
2.0210	KVTKYLPLDK	10	HBV	ayw	POL	721	3,11			0.027	0.053	
1.1148	STRHGDKSFR	10	HBV	adw	POL	792	3,11			0.0057	0.038	
1.0935	VLSCWWLQFR	10	HBV	adw	POL	923	3,11			0.029	0.0087	
1.0781	NVTKYLPLDK	10	HBV	adw	POL	721	3,11			<0.0004	0.023	
1.1092	RVCCQLDPAR	10	HBV	adr	'X'	1422	3,11			0.0019	0.023	
1.0793	SLGIHLNPQK	10	HBV	adw	POL	1179	3,11			0.017	0.014	
1.0909	YLVSFGVWIR	10	HBV	adr	CORE	508	3,11			0.015	0.0027	

Peptide	Sequence	AA	Virus	Strain	Molecule	Pos.	Motif	A1	A2.1	A3.2	A11	A24
2.0207	FVGPLTVNEK	10	HBV	ayw	POL	698	3,11			0.0057	0.015	
1.0535	YVCPLTVNEK	10	HBV	adr	POL	669	3,11			0.0069	0.014	
1.1075	RLADEGLNRR	10	HBV	adr	POL	601	3,11			0.013	0.0004	
1.1086	IVLKLKQCFR	10	HBV	adr	POL	1185	3,11			0.013	0.0024	
1.0773	PIPSSWAFAK	10	HBV	adw	ENV	314	3,11			<0.0003	0.010	
1.0778	LTVNENRRLK	10	HBV	adw	POL	702	3,11			0.0025	0.0095	

Peptide	Sequence	AA	Virus	Strain	Molecule	Pos.	Motif	A1	A2.1	A3.2	A11	A24
1.0118	CTCGSSDLY	9	HCV		LORF	1123	1	3.0		0	0.010	
1.0112	NIVDVQYLY	9	HCV		NS1/ENV2	697	1	0.60		0	0.010	
2.0034	VQDCNCSIY	9	HCV			302	1	0.54		0.0005	0.0003	
2.0035	LTPRCMVDY	9	HCV			605	1	0.078				
1.0145	RVCEKMALY	9	HCV		LORF	2588	1	0.053				
1.0140	DVVCCSMSY	9	HCV		LORF	2416	1	0.039				
2.0036	FTIFKIRMY	9	HCV			626	1	0.012				
1.0509	GLSAFSLHSY	10	HCV		LORF	2888	1	0.41	0.0002	0.013	0.0034	0.0002
1.0489	TLHGPTPLLY	10	HCV		LORF	1617	1	0.30		0.11	0.0024	
2.0037	EYVLLLFLL	9	HCV			719	24					1.4
2.0169	MYVGGVEHRL	10	HCV			633	24					0.026
2.0170	EYVLLLFLLL	10	HCV			719	24					0.010
1.0139	SVPAEILRK	9	HCV		LORF	2269	3,11			0.016	0.87	
1.0955	QLFTFSPRR	9	HCV		ENV1	290	3,11			0.75	0.033	
1.0090	RLGVRATRK	9	HCV		CORE	43	3,11			0.74	0.16	
1.0123	LIFCHSKKK	9	HCV		LORF	1391	3,11			0.54	0.19	
1.0122	HLIFCHSKK	9	HCV		LORF	1390	3,11			0.25	0.010	
1.0952	KTSERSQPR	9	HCV		CORE	51	3,11			0.16	0.064	
1.0120	AVCTRGVAK	9	HCV		LORF	1183	3,11			0.016	0.038	
1.0143	EVFCVQPEK	9	HCV		LORF	2563	3,11			0.0019	0.033	
1.0137	ITRVESENK	9	HCV		LORF	2241	3,11			0.015	0.0079	
1.0957	CIITSLTGR	9	HCV		LORF	1042	3,11			0.0095	0.011	
1.0496	GVAGALVAFK	10	HCV		LORF	1858	3,11			0.87	1.1	
1.0480	HLHAPTGSGK	10	HCV		LORF	1227	3,11			0.57	0.0051	
1.1062	RMYVGGVEHR	10	HCV		NS1/ENV2	632	3,11			0.27	0.012	
1.0485	HLIFCHSKKK	10	HCV		LORF	1390	3,11			0.27	0.025	
1.0484	TLGFGAYMSK	10	HCV		LORF	1261	3,11			0.17	0.13	
1.1067	GVCIYLLPNR	10	HCV		LORF	3002	3,11			0.0029	0.032	
1.1063	LLFLLLADAR	10	HCV		NS1/ENV2	723	3,11			0.015	0	

Peptide	Sequence	AA	Virus	Strain	Molecule	Pos.	Motif	A1	A2.1	A3.2	A11	A24
1.0014	FRDYVDRFY	9	HIV		GAG	298	1	0.090				
2.0129	IYQYMDDLY	9	HIV			875	1	0.064				
1.0028	TVLDVGDAY	9	HIV		POL	802	1	0.018		<0.0002	0.0056	
1.0412	VTVLDVGDAY	10	HIV		POL	801	1	0.28		0	0.0004	
1.0415	VIYQYMDDLY	10	HIV		POL	874	1	0.25		0.0007	0.0090	
2.0252	VTVLDVGDAY	10	HIV			801	1	0.088				
1.0431	EVNIVTDSQY	10	HIV		POL	1187	1	0.053				
1.0441	LVAVHVASGY	10	HIV		POL	1329	1	0.039				
1.0442	PAETGQETAY	10	HIV		POL	1345	1	0.013				
2.0251	ISKIGPENPY	10	HIV			742	1	0.013				
2.0255	QMAVFIHNFK	10	HIV			1,432	3			0.61	0.64	
2.0064	RYLKDQQLL	9	HIV			2,778	24					0.76
2.0134	RYLKDQQLL	9	HIV			2,778	24					0.32
2.0065	TYQIYQEPF	9	HIV			1,033	24					0.30
2.0131	TYQIYQEPF	9	HIV			1,033	24					0.20
2.0063	IYQEPFKNL	9	HIV			1,036	24					0.052
2.0132	IYQEPFKNL	9	HIV			1,036	24					0.033
2.0066	IYQYMDDLY	9	HIV			875	24					0.013
2.0247	IYKRWIILGL	10	HIV			266	24					0.017
2.0190	IYKRWIILGL	10	HIV			266	24					0.014
2.0249	LYPLASLRSL	10	HIV			506	24					0.014
1.0069	KLAGRWPVK	9	HIV		POL	1358	3,11			2.7	0.069	
1.0944	AVFIHNFKR	9	HIV		POL	1434	3,11			0.17	1.8	
1.0032	AIFQSSMTK	9	HIV		POL	853	3,11			1.1	0.96	
1.0046	IVIWGKTPK	9	HIV		POL	1075	3,11			0.085	0.37	
1.0079	KLTEDRWNK	9	HIV		VIF	1712	3,11			0.013	0.27	
1.0027	GIPHPAGLK	9	HIV		POL	788	3,11			0.23	0.065	
1.0059	QIIEQLIKK	9	HIV		POL	1215	3,11			0.0091	0.16	
1.0939	KIWPSYKGR	9	HIV		GAG	443	3,11			0.12	0.0005	
1.0072	IIATDIQTK	9	HIV		POL	1458	3,11			0.025	0.098	
1.0036	MGYELHPDK	9	HIV		POL	925	3,11			0.064	0.096	
1.0062	YLAWVPAHK	9	HIV		POL	1227	3,11			0.077	0.057	
1.0938	KIWPSHKGR	9	HIV		GAG	443	3,11			0.077	<0.0005	
1.0047	FVNTPPLVK	9	HIV		POL	1111	3,11			0.012	0.066	
1.0024	NTPVFAIKK	9	HIV		POL	752	3,11			0.033	0.060	
1.0080	TVQCTHGIK	9	HIV		ENV	2420	3,11			0.0021	0.046	
1.0013	ILDIRQGPK	9	HIV		GAG	287	3,11			0.042	0.0048	

Peptide	Sequence	AA	Virus	Strain	Molecule	Pos.	Motif	A1	A2.1	A3.2	A11	A24
1.0015	RDYVDRFYK	9	HIV		GAG	299	3,11			0.0007	0.040	
1.0058	GIIQAQPDK	9	HIV		POL	1199	3,11			<0.0009	0.040	
1.0064	VLFLDGIDK	9	HIV		POL	1254	3,11			0.038	0.032	
1.0026	LVDFRELNK	9	HIV		POL	769	3,11			0.011	0.030	
1.0078	KVVPRRKAK	9	HIV		POL	1513	3,11			0.029	0.0039	
1.0942	MTKILEPFR	9	HIV		POL	859	3,11			<0.0008	0.016	
1.0463	TVYYGVPVWK	10	HIV		ENV	2185	3,11			3.8	7.8	
1.0418	TVQPIVLPEK	10	HIV		POL	935	3,11			0.16	5.6	
1.0447	AVFIHNFKRK	10	HIV		POL	1434	3,11			0.66	0.85	
1.0437	KVLFLDGIDK	10	HIV		POL	1253	3,11			0.36	0.78	
1.0408	KLVDFRELNK	10	HIV		POL	768	3,11			0.51	0.090	
1.0403	KLKPGMDGPK	10	HIV		POL	706	3,11			0.39	0.076	
1.0395	FLGKIWPSYK	10	HIV		GAG	440	3,11			0.32	0.024	
1.1056	KIQNFRVYYR	10	HIV		POL	1474	3,11			0.032	0.21	
1.0410	GIPHPAGLKK	10	HIV		POL	788	3,11			0.011	0.17	
1.0426	LVKLWYQLEK	10	HIV		POL	1117	3,11			0.056	0.082	
1.0398	MIGGIGGFIK	10	HIV		POL	642	3,11			0.0099	0.055	
1.0413	MTKILEPFRK	10	HIV		POL	859	3,11			0.015	0.038	
1.0453	VVIQDNSDIK	10	HIV		POL	1504	3,11			<0.0005	0.021	
1.0394	FLGKIWPSHK	10	HIV		GAG	440	3,11			0.020	0.0013	
1.1059	IVQQQNNLLR	10	HIV		ENV	2741	3,11			0.0024	0.019	
1.0417	FTTPDKKHQK	10	HIV		POL	909	3,11			<0.0002	0.015	
1.0405	LVEICTEMEK	10	HIV		POL	729	3,11			0.0002	0.012	
1.0392	LVQNANPDCK	10	HIV		GAG	327	3,11			<0.0002	0.011	

Peptide	Sequence	AA	Virus	Strain	Molecule	Pos.	Motif	A1	A2.1	A3.2	A11	A24
1.0225	ISEYRHYCY	9	HPV	16	E6	80	1	7.8		0.0011	0.036	
1.0230	QAEPDRAHY	9	HPV	16	E7	44	1	0.021		<0.0002	<0.0002	
1.0610	LQDIEITCVY	10	HPV	18	E6	25	1	0.25		0.0056	0.012	
2.0159	YSKISEYRHY	10	HPV	16	E6	77	1	0.17		<0.0009	0	
2.0162	YSKISEYRHY	10	HPV	16	E6	77	1	0.11		<0.0009	0	
1.0599	HGDTPTLHEY	10	HPV	16	E7	2	1	0.087		<0.0002	<0.0002	
1.0601	QPETTDLYCY	10	HPV	16	E7	16	1	0.033				
1.0913	IHDIILECVY	10	HPV	16	E6	30	1	0.032				
1.0594	AVCDKCLKFY	10	HPV	16	E6	68	1	0.0095		0.0052	0.019	
2.0160	YSRIRELRHY	10	HPV	18	E6	72	1	0.018		<0.0002	<0.0002	
2.0164	YSRIRELRHY	10	HPV	18	E6	72	1	0.012				
2.0161	LLIRCLRCQK	10	HPV	18	E6	101	3			0.081	0.078	
2.0032	HTMLCMCCK	9	HPV	18	E7	59	11			0.020	0.079	
2.0029	VYCKTVLEL	9	HPV	18	E6	33	24					0.33
2.0027	CYSLYGTTL	9	HPV	16	E6	87	24					0.057
2.0024	VYDFAPRDL	9	HPV	16	E6	49	24					0.032
2.0031	LYNLLIRCL	9	HPV	18	E6	98	24					0.019
2.0030	VYGDTLEKL	9	HPV	18	E6	85	24					0.010
1.0239	SVYGDTLEK	9	HPV	18	E6	84	3,11			0.39	2.3	
1.0243	SVYGDTLEK	9	HPV	18	E6	84	3,11			0.55	1.1	
1.0244	SVYGDTLEK	9	HPV	18	E6	84	3,11			0.70	0.95	
1.0226	TTLEQQYNK	9	HPV	16	E6	93	3,11			0.010	0.67	
1.0241	SIPHAACHK	9	HPV	18	E6	59	3,11			0.0094	0.25	
1.0237	SIPHAACHK	9	HPV	18	E6	59	3,11			0.017	0.12	
1.0233	IVCPICSQK	9	HPV	16	E7	89	3,11			0.035	0.023	
1.0997	KLRHLNEKR	9	HPV	18	E6	117	3,11			0.025	<0.0005	
1.0234	LIRCLRCQK	9	HPV	18	E6	102	3,11			0.019	0.0012	
1.0853	IILECVYCK	9	HPV	16	E6	33	3,11			0.0016	0.019	
1.0999	CIDFYSRIR	9	HPV	18	E6	68	3,11			0.017	0.0018	
1.0998	CIDFYSRIR	9	HPV	18	E6	68	3,11			0.010	0.0009	
1.0596	GTTLEQQYNK	10	HPV	16	E6	92	3,11			0.010	0.98	
1.0606	LLIRCLRCQK	10	HPV	18	E6	101	3,11			0.076	0.29	
1.0598	LLIRCINCQK	10	HPV	16	E6	106	3,11			0.12	0.24	
1.0629	LLIRCLRCQK	10	HPV	18	E6	101	3,11			0.16	0.11	
1.0614	LTEVFEFAFK	10	HPV	18	E6	41	3,11			0.0009	0.11	
1.0605	GIVCPICSQK	10	HPV	16	E7	88	3,11			0.0017	0.060	
1.0625	LTEVFEFAFK	10	HPV	18	E6	41	3,11			0.0012	0.041	
1.0591	DIILECVYCK	10	HPV	16	E6	32	3,11			0.0065	0.021	
1.1101	KLRHLNEKRR	10	HPV	18	E6	117	3,11			0.013	0	
1.1095	CVYCKQQLLR	10	HPV	16	E6	37	3,11			0.011	0.0059	

Peptide	Sequence	AA	Virus	Strain	Molecule	Pos.	Motif	A1	A2.1	A3.2	A11	A24
2.0020	EVDPIGHLY	9	MAGE	3		161	1	18		0.0002	0.0009	
3.0172	EADPTSNTY	9	MAGE	5/51		161	1	9.9		0.0006	0.0006	0
1.0258	TQDLVQEKY	9	MAGE	1		240	1	2.1		0	0.0002	
3.0173	EVDPIGHVY	9	MAGE	6		161	1	1.9		<0.0002	<0.0002	0
1.0254	EADPTGHSY	9	MAGE	1		161	1	1.1		0	0	
1.0259	LVQEKYLEY	9	MAGE	1		243	1	0.42		0.0013	0.053	
6.0053	TSYVKVLEY	9	MAGE	1	new	275	1	0.099				
2.0009	SSLPTTMNY	9	MAGE	3		9	1	0.055				
2.0011	GSVVGNWQY	9	MAGE	3		77	1	0.050				
2.0008	SSPSTTINY	9	MAGE	2		9	1	0.043				
1.0252	MLESVIKNY	9	MAGE	1		128	1	0.011				
2.0147	ASSLPTTMNY	10	MAGE	3		8	1	2.6		<0.0009	0.033	
2.0167	LTQDLVQEKY	10	MAGE	1		239	1	1.2		<0.0009	0.0073	
6.0114	ETSYVKVLEY	10	MAGE	1	new	274	1	0.56				
2.0141	ASSPSTTINY	10	MAGE	2		8	1	0.17		<0.0009	0.026	
1.0648	DLVQEKYLEY	10	MAGE	1		242	1	0.044				
6.0065	TSYVKVLEY	9	MAGE	1	new	275	3			0.71	0.010	
4.0119	TTINFTRQR	9	MAGE	1		66	3			0.043	0.37	
6.0064	ALAETSYVK	9	MAGE	1	new	271	3			0.31	0.36	
4.0132	LTQDLVQEK	9	MAGE	1		239	3			<0.0003	0.14	
6.0062	LVQEKYLEY	9	MAGE	1	new	243	3			0.0026	0.034	
4.0131	HSAYGEPRK	9	MAGE	1		229	3			0.014	0.0009	
4.0122	LFRAVITKK	9	MAGE	1		97	3			0.011	0.0005	
6.0124	EVRPFFPSLR	10	MAGE	1	new	290	3			0.43	0.0089	
4.0161	ADLVGFLLLK	10	MAGE	1		107	3			0.35	0.29	
4.0160	ESLFRAVITK	10	MAGE	1		95	3			0.14	0.088	
6.0119	DLVQEKYLEY	10	MAGE	1	new	242	3			0.032	0.0051	
6.0123	YVIKVSARVR	10	MAGE	1	new	283	3			0.019	0.0009	
4.0168	LSVMEVYDGR	10	MAGE	1		218	3			<0.0003	0.012	
4.0163	KAEMLESVIK	10	MAGE	1		125	3			<0.0003	0.0097	
6.0125	RALAETSYVK	10	MAGE	1	new	270	11			0.18	0.24	
2.0010	NYPLWSQSY	9	MAGE	3		16	24					0.027
2.0165	NYKHCFPEIF	10	MAGE	1		135	24					0.25
2.0151	LYIPATCLGL	10	MAGE	3		115	24					0.048
6.0126	SYVKVLEYVI	10	MAGE	1	new	276	24					0.036
1.0248	SLFRAVITK	9	MAGE	1		96	3,11			4.1	2.7	
1.1006	SVMEVYDGR	9	MAGE	1		219	3,11			0.0093	1.3	
1.1004	TTINFTRQR	9	MAGE	1		66	3,11			0.016	1.0	
1.0257	LTQDLVQEK	9	MAGE	1		239	3,11			0.0002	0.38	
1.0634	SLFRAVITKK	10	MAGE	1		96	3,11			1.2	0.98	
1.0647	LLTQDLVQEK	10	MAGE	1		238	3,11			0.0004	0.16	
1.0640	MLESVIKNYK	10	MAGE	1		128	3,11			0.14	0.027	
1.0644	LLGDNQIMPK	10	MAGE	1/3		182	3,11			0.020	0.011	
1.0630	SLEQRSLHCK	10	MAGE	1		2	3,11			0.015	0.015	

Peptide	Sequence	AA	Virus	Strain	Molecule	Pos.	Motif	A1	A2.1	A3.2	A11	A24
1.0281	GSDCTTIHY	9	p53			226	1	29.5		0.0010	0.029	
1.0667	GTAKSVTCTY	10	p53			117	1	0.33	0	0.023	0.049	0
1.0672	RVEGNLRVEY	10	p53			196	1	0.022		0.0014	0.0020	
1.0278	RVRAMAIYK	9	p53			156	3,11			1.5	0.73	
1.0276	CTYSPALNK	9	p53			124	3,11			0.46	1.1	
1.0285	NTSSSPQPK	9	p53			311	3,11			0.0009	0.095	
1.0284	RTEEENLRK	9	p53			283	3,11			0.0015	0.091	
1.0287	ELNEALELK	9	p53			343	3,11			0.020	0.0052	
1.0678	RTEEENLRKK	10	p53			283	3,11			3.3	0.0080	
1.1113	KTYQGSYGFR	10	p53			101	3,11			2.6	0.88	
1.1115	VVRRCPHHER	10	p53			172	3,11			0.099	0.0017	
1.0679	NTSSSPQPKK	10	p53			311	3,11			0.0035	0.054	
1.1121	RVCACPGRDR	10	p53			273	3,11			0.014	0.011	
1.1116	GLAPPQHLIR	10	p53			187	3,11			0.013	0.0006	

Peptide	Sequence	AA	Virus	Strain	Molecule	Pos.	Motif	A1	A2.1	A3.2	A11	A24
3.0175	KCEYFVEMY	9	PAP			322	1	3.4		<0.0002	0.0002	0
3.0174	LCEYIRKRY	9	PAP			81	1	0.78		<0.0002	0.0002	0
3.0166	ASCHLTELY	9	PAP			311	1	0.77	<0.0002	<0.0002	0.055	0
3.0163	ESYKHEQVY	9	PAP			95	1	0.098		<0.0002	0.0002	0
3.0237	LSELSLLSLY	10	PAP			238	1	14		0.0026	0.0004	0
3.0235	LSELSLLSLY	10	PAP			238	1	12		0.0005	0.0004	0
3.0236	LTQLGMEQHY	10	PAP			70	1	0.62	0.0005	0.015	0.0024	0.0022
3.0238	KGEYFVEMYY	10	PAP			322	1	0.018		0.0057	0.089	
3.0230	LVNEILNHMK	10	PAP			263	3			0.056	0.12	
3.0158	ATQIPSYKK	9	PAP			274	11			0.10	1.2	
3.0231	ETLKSEEFQK	10	PAP			170	11			<0.0004	0.014	
3.0161	LYFEKGEYP	9	PAP			318	24					2.5
3.0160	LYCESVHNF	9	PAP			213	24					0.44
3.0159	PYKDFIATL	9	PAP			183	24					0.11
3.0162	VYNGLLPPY	9	PAP			302	24					0.032
3.0232	PYASCHLTEL	10	PAP			309	24					0.024

Peptide	Sequence	AA	Virus	Strain	Molecule	Pos.	Motif	A1	A3.2	A11	A24
1.0270	ALPERPSLY	9	PSA			231	1	0.011			
2.0157	VSHSFPHPLY	10	PSA			88	1	0.15	<0.0003	0.0015	
1.0265	PLYDMSLLK	9	PSA			95	3.11		0.24	0.037	
1.0273	VVHYRKWIK	9	PSA			242	3.11		0.0072	0.083	
1.0272	YTKVVHYRK	9	PSA			239	3.11		0.0006	0.056	
1.1009	SLLKNRFLR	9	PSA			100	3.11		0.0036	0.087	
1.0260	IVGGWECEK	9	PSA			21	3.11		0.041	0.019	
1.0269	QVHPQKVTK	9	PSA			182	3.11		0.0080	0.014	
1.1112	SLYTKVVHYR	10	PSA			237	3.11		0.29	0.23	
1.0663	LTAAHCIRNK	10	PSA			57	3.11		0.14	0.083	
1.0661	IIVGGWECEK	10	PSA			20	3.11		0.046	0.067	
1.0662	KVVHYRKWIK	10	PSA			241	3.11		0.045	0.065	
1.1111	VTKFMLCAGR	10	PSA			188	3.11		0.0003	0.012	
3.0108	MLLRLSEPA	9	PSA			118	Random				

Table 5

Sequence	Size	Antigen	Strain	Molecule	Freq	Pos.	Motif	A01	A03	A11	A24
								Bind.	Bind.	Bind.	Bind.
EDTPIGHLY	9	MAGE3a	3	analog		161	A01	12.5000			
AVDPIGHLY	9	MAGE3a	3	analog		161	A01	8.0000			
EVDPIAHLY	9	MAGE3a	3	analog		161	A01	5.5000			
FSPAFDNLYY	10	HER-2/neu				1213	A01	5.5000	0.0005	0.0010	
EVDAIGHLY	9	MAGE3a	3	analog		161	A01	5.3500			
EVDPIGALY	9	MAGE3a	3	analog		161	A01	5.0000			
EVDPIGHAY	9	MAGE3a	3	analog		161	A01	4.6500			
EADPIGHLY	9	MAGE3a	3	analog		161	A01	3.4500			
EVDPTGHLY	9	MAGE3a	3	analog		161	A01	2.9500			
EVDPIGHSY	9	MAGE3a	3	analog		161	A01	2.6667			
EVDPAGHLY	9	MAGE3a	3	analog		161	A01	2.4000			
EVDPASNTY	9	MAGE	4			161	A01	1.5000			
PLSEDQLLY	9	PAP				147	A01	1.2000	0.0005	0.0001	
LSAFSLHSY	9	HCV				2889	A01	0.8100	0.0002	0.0002	
IPSYKKLIMY	10	PAP				277	A01	0.5650			
YASCHLTELY	10	PAP				310	A01	0.5467	0.0003	0.0002	
EVDPIGHLA	9	MAGE3a	3	analog		161	A01	0.3300			
CMQIAKGMSY	10	HER-2/neu				826	A01	0.2967	0.0003	0.0001	
VGSDCTTIHY	10	p53				225	A01	0.2600	0.0003	0.0003	
EVAPIGHLY	9	MAGE3a	3	analog		161	A01	0.1800			

Table 5

Sequence	Size	Antigen	Strain	Molecule	Freq	Pos.	Motif	A01 Bind.	A03 Bind.	A11 Bind.	A24 Bind.
ESMPNPEGRY	10	HER-2/neu				280	A01	0.1800	0.0003	0.0003	
ASCVTACPY	9	HER-2/neu				293	A01	0.0552	0.0008	0.0074	
FSPAFDNLY	9	HER-2/neu				1213	A01	0.0425	0.0002	0.0002	
ASPLDSTFY	9	HER-2/neu				997	A01	0.0290	0.0002	0.0004	
RGTQLFENDY	10	HER-2/neu				103	A01	0.0205	0.0003	0.0015	
PASPLDSTFY	10	HER-2/neu				996	A01	0.0148	0.0003	0.0001	
PSQKTYQGSY	10	p53				98	A01	0.0140	0.0003	0.0003	
KSTKVPAAY	9	HCV				1236	A01	0.0134	0.0009	0.0001	
DSSVLCECY	9	HCV				1513	A01	0.0110	0.0002	0.0003	
KISEYRHYCY	10	HPV	16	E6		79	A01	0.0090	0.0043	0.0038	
NLYVSLMLLY	10	HBV	adw	POL	20	1088	A01	0.0090			
GTRVRAMAIY	10	p53				154	A01/03	0.0027	0.0365	0.0002	
LTCGFADLMGY	11	HCV				126	A01/11	2.4500	0.0003	0.0120	0.0001
VMAGVGSPY	9	HER-2/neu				773	A01/A03	0.0400	0.0575	0.0079	
TLWKAGILY	9	HBV	adr	POL	100	724	A03	0.0017	0.2667	0.0016	
KLNWASQIY	9	HIV		POL		958	A03	0.0070	0.1160	0.0006	
LVGPLLLKY	9	MAGE1	1			109	A03	0.0033	0.0563	0.0012	
ILRGTSFVY	9	HBV	adr	POL	80	1345	A03	0.0017	0.0440	0.0002	
RVLOGLPREY	10	HER-2/neu				545	A03	0.0015	0.0350	0.0050	

Table 5

Sequence	Size	Antigen	Strain	Molecule	Freq	Pos.	Motif	A01	A03	A11	A24
								Bind.	Bind.	Bind.	Bind.
QLVTQLMPY	9	HER-2/neu				795	A03	0.0024	0.0112	0.0039	
GLNKIVRMY	9	HIV		GAG		274	A03	0.0017	0.0103	0.0002	
LLGDNQVMPK	10	MAGE2	2			182	A03		0.0093	0.0014	
QVRDQAEHLK	10	HIV		POL		1419	A03		0.0089	0.0093	
LVSAGIRK	8	HIV	con			1246	A03		0.0091	0.0054	
VTDRGRQK	8	HIV	con			1153	A03		0.0090	0.0065	
TVFDAKRLIGR	11	HLA-Aw68 endogenous peptide sequences					A03/11		0.1050	1.3000	
KTGGPIYKR	9	HLA-Aw68 endogenous peptide sequences					A03/11		0.0340	0.8200	
SLYTKVVHY	9	PSA				237	A03/11	0.0017	0.6750	0.0140	
AVAAVAARR	9	HLA-Aw68 endogenous peptide sequences					A03/11		0.1600	0.0825	
KIQNFRVYY	9	HIV		POL		1474	A03/11	0.0056	0.1190	0.1350	
EMLESVIKNYK	11	MAGE1				127	A03/11		0.0087	0.0099	
EVAPPEYHRK	10	HLA-Aw68 endogenous peptide sequences					A11		0.0008	0.0575	
ETAYFLLK	8	HIV	consensus			1351	A11		0.0037	0.0425	
RWGLLLALL	9	HER-2/neu				8	A24				1.2567
PYVSRLLGI	9	HER-2/neu				780	A24				0.1650
VYMIMVKCW	9	HER-2/neu				951	A24				0.1640
AYSLTLQGL	9	HER-2/neu				440	A24				0.1250
SYGVTVWEL	9	HER-2/neu				907	A24				0.1200
LYISAWPDSL	10	HER-2/neu				410	A24				0.0835
VWSYGVTVW	9	HER-2/neu				905	A24				0.0800

Table 5

Sequence	Size	Antigen	Strain	Molecule	Freq	Pos.	Motif	A01	A03	A11	A24
								Bind.	Bind.	Bind.	Bind.
SYGVTVWELM	10	HER-2/neu				907	A24				0.0630
QYLAGLSTL	9	HCV				1777	A24				0.0475
TYLPTNASL	9	HER-2/neu				63	A24				0.0375
EYLVSFGVWI	10	HBV		NUC	90	117	A24				0.0335
KFMLCAGRW	9	PSA				190	A24				0.0305
WFHISCLTF	9	HBV		NUC	90	102	A24				0.0300
TYSTYGKFL	9	HCV				1296	A24				0.0225
VYMIMVKCWM	10	HER-2/neu				951	A24				0.0218
RFRELVSEF	9	HER-2/neu				968	A24				0.0180
CYGLGMEHL	9	HER-2/neu				342	A24				0.0176
QYSPGQRVEF	10	HCV				2614	A24				0.0175
KWMALESIL	9	HER-2/neu				887	A24				0.0149
EYLVPQQGFF	10	HER-2/neu				1022	A24				0.0120
RYSEDPTVPL	10	HER-2/neu				1111	A24				0.0117
RFTHQSDVW	9	HER-2/neu				898	A24				0.0107

Table 5

Sequence	AA	Mage Strain	Mol.	Pos.	Motif	A1	A2.1	A3.2	A11	A24
DLVGFLLLK	9	1		108	3,11			0.0040	0.0014	
QLVFGIDVK	9	1		152	3,11			0.0019	0.0051	
SLEQRSLHCK	10	1		2	3,11			0.015	0.015	
SLFRAVITKK	10	1		96	3,11			1.2	0.98	
DLVGFLLLKY	10	1		108	1	0.0068		0.0069	0.0009	
MLESVIKNYK	10	1		128	3,11			0.14	0.027	
WEELSVMEVY	10	1		215	1	<0.0009		<0.0002	<0.0002	
VYDGREHSAY	10	1		223	1	<0.0009				
LVGFLLLKY	9	1		109	1	0.0033		0.056	0.0012	
LVTCLGLSY	9	1		171	1	0.0084		0.0014	<0.0002	
VLVTCLGLSY	10	1		170	1	0.0048	0	0.0013	0.0007	
FLLLKYRAR	9	1/2/3		112	3,11			0.0007	<0.0005	
PTTINFTRQR	10	1		65	3,11			<0.0002	0.0033	
LVGFLLLKYR	10	1		109	3,11			0.0034	0.0023	
EKYLEYGRCR	10	1		246	3,11			<0.0002	0	
ELVHFLLLK	9	2/3		108	3			0.0045	0.0011	
AYGEPRKLL	9	1		231	24					0.0007
SYVLVTCLGL	10	1		168	24		0.0006			0.0051
EVVPISHLY	9	2		161	1	0.0028		<0.0002	<0.0002	
EVVRIGHLY	9	21		161	1	0.0002				
EVDPASNTY	9	4		161	1	0.0005				
EADPTSNTY	9	5/51		161	1	9.9		0.0006	0.0006	0

Table 5

Sequence	AA	Mage Strain	Mol.	Pos.	Motif	A1	A2.1	A3.2	A11	A24
EVDPIGHVY	9	6		161	1	1.9		<0.0002	<0.0002	0
EMLESVIK	8	1		127	3			<0.0003	0	
LVFGIDVK	8	1		153	3			0.0035	0.0037	
GVQGPSLK	8	1		266	3			<0.0003	0.0063	
VMEVYDGR	8	1		220	3			<0.0003	0.0007	
VQEKYLEY	8	1		244	1	0.0018				
AYGEPRKL	8	1		231	24					0.0017
VKEADPTGHSY	11	1		159	1	<0.0003				
IWEELSVMEVY	11	1		214	1	<0.0003				
EMLESVIKNYK	11	1		127	3		0.0087	0.0099		
EADPTSHTY	9	analog		161	1	0.68				
EVDPTSNTY	9	analog		161	1	1.8				
EALEAQQEA	9	1		14	2.1		0	<0.0002	0	
MSLEQRSLH	9	1		1	3			0.0025	0.0003	
QSPQGASAF	9	1		56	3			0.0004	0	
SAFPTTINF	9	1		62	3			<0.0003	0	0.0003
TSCILESLF	9	1		90	3			<0.0003	0	
SCILESLFR	9	1		91	3			<0.0003	0.0026	
LFRAVITKK	9	1		97	3			0.011	0.0005	
VGFLLLKYR	9	1		110	3			0.0044	0.0051	
ESVIKNYKH	9	1		130	3			<0.0003	0	
VIKNYKHCF	9	1		132	3			<0.0003	0	

Table 5

Sequence	AA	Mage Strain	Mol.	Pos.	Motif	A1	A2.1	A3.2	A11	A24
ASESLQLVF	9	1,2		147	3			<0.0003	0	
LGDNQIMPK	9	1		183	3			0.0007	0.0048	
VMIAMEGGH	9	1		200	3			<0.0003	0	
YDGREHSAY	9	1		224	3			<0.0003	0	
LTQDLVQEK	9	1		239	3			<0.0003	0.14	
CGVQGPSLK	9	1		265	3			<0.0003	0.0037	
EMLESVIKNY	10	1		127	1	0.0006		<0.0002	<0.0002	0
KEADPTGHSY	10	1		160	1	<0.0005		<0.0002	<0.0002	
ASAFPTTINF	10	1		61	3			<0.0003	<0.0002	
AFPTTINFTR	10	1		63	3			<0.0003	0.0003	
PTTINFTRQR	10	1		65	3			<0.0003	0.0002	
STSCILESLF	10	1		89	3			<0.0003	<0.0002	
GFLLLKYRAR	10	1		111	3			0.0019	0.0008	
KAEMLESVIK	10	1		125	3			<0.0003	0.0097	
SVIKNYKHCF	10	1		131	3			<0.0003	<0.0002	
KASESLQLVF	10	1		146	3			<0.0003	<0.0002	0.0012
DVKEADPTGH	10	1		158	3			<0.0003	<0.0002	
LVMIAMEGGH	10	1		199	3			0.0008	0.0005	
LSVMEVYDGR	10	1		218	3			<0.0003	0.012	
VMEVYDGREH	10	1		220	3			<0.0003	0.0002	0
YGRCRTVIPH	10	1		251	3			<0.0003	<0.0002	
SCGVQGPSLK	10	1		264	3			0.0005	0.0089	

Table 5

Sequence	AA	Mage Strain	Mol.	Pos.	Motif	A1	A2.1	A3.2	A11	A24
VPDSDPARY	9	1	new	254	1	0.0038				
QVPDSDPAR	9	1	new	254	3			<0.0003	0.0002	
VIKVSARVR	9	1	new	284	3			0.0016	0	
PSLREAALR	9	1	new	296	3			<0.0003	0	
EFLWGPRAL	9	1	new	264	24					0.0006
ETSYVKVLEY	10	1	new	274	1	0.56				
LVQEKYLEYR	10	1	new	243	3			0.0008	0.0043	
QVPDSDPARY	10	1	new	254	3			0.0014	0.0003	
YVKVLEYVIK	10	1	new	277	3			0.0029	0.0015	
YVIKVSARVR	10	1	new	283	3			0.019	0.0009	
RALAETSYVK	10	1	new	270	11			0.18	0.24	
SYVKVLEYVI	10	1	new	276	24					0.036
FFPSLREAAL	10	1	new	294	24					0.0044
SVIKNYK	7	1 N	POL	131	3,11			0.0006	0.0028	
PVTKAEMLESVIK	13	1 n	E6	122	3,11			<0.0003	0	
ETSYVKVLEYVIK	13	1 n	E6	273	3,11			0.0044	0.0003	
ITKKVADLVGFLLLK	15	1 n	POL	102	3,11			0.40	1.0	
VTKAEMLESVIKNYK	15	1 n	POL	123	3,11			0.024	0.053	
VVGNWQYFFPVIFSK	15	3	POL	79	3,11			1.6	0.34	
PRALAETSY	9	1	new	268	1	<0.0018		<0.0003	<0.0002	
FATCLGLSY	9	3		171	1	0.038		<0.0003	0.0004	
LEQRSLHCK	9	1	new	3	3			<0.0002	0	

Table 5

Sequence	AA	Mage Strain	Mol.	Pos.	Motif	A1	A2.1	A3.2	A11	A24
AEMLESVIK	9	1	new	126	3			<0.0002	0.0011	
LESVIKNYK	9	1	new	129	3			<0.0002	0.0018	
EELSVMEVY	9	1	new	216	3			<0.0002	0	
MEVYDGREH	9	1	new	221	3			<0.0002	0	
DSDPARYEF	9	1	new	256	3			<0.0002	0	
KVSARVRFF	9	1	new	285	3			0.0005	0	
VSARVRFFF	9	1	new	286	3			0.0003	0.0026	
HSPQGASSF	9	2		56	3			<0.0002	0	
TTINYTLWR	9	2		66	3			0.089	1.1	
QEEEGPRMF	9	2		83	3			<0.0002	0	
MFPDLESEF	9	2		90	3			<0.0002	0	0.014
SEFQAAISR	9	2		96	3			<0.0002	0.0001	
EFQAAISRK	9	2		97	3			<0.0002	0.0002	
LVHFLLLKY	9	2,3		109	3			0.043	0.010	
AEMLESVLR	9	2		126	3			<0.0002	0	
SVLRNCQDF	9	2		131	3			<0.0002	0	
VLRNCQDFF	9	2		132	3			<0.0002	0	
DFFPVIFSK	9	2		138	3			<0.0002	0.0022	
VIFSKASEY	9	2		142	3			0.081	0.033	
VVEVVPISH	9	2		159	3			0.0007	0.010	
LGDNQVMPK	9	2		183	3			<0.0002	0.0061	
EGDCAPEEK	9	2,3		205	3			<0.0002	0	

Table 5

Sequence	AA	Mage Strain	Mol.	Pos.	Motif	A1	A2.1	A3.2	A11	A24
QEEEGPSTF	9	3		83	3			<0.0002	0	
TFPDLESEF	9	3		90	3			<0.0002	0	0.0049
SEFQAALSR	9	3		96	3			<0.0002	0	
EFQAALSRK	9	3		97	3			<0.0002	0.0001	
SVVGNWQYF	9	3		131	3			<0.0002	0	
VVGNWQYFF	9	3		132	3			0.0022	0.0021	
YFFPVIFSK	9	3		138	3			0.0020	0.027	
ASSSLQLVF	9	3		147	3			0.0011	0.0089	
LMEVDPIGH	9	3		159	3			<0.0002	0	
IIVLAIIAR	9	3		196	3			0.0069	0.0011	
VQEKYLEYR	9	1		244	11			<0.0002	0	
SNQEEEGPR	9	2		81	11			<0.0002	0	
NYKHCFPEI	9	1	new	135	24					4.8
IFGKASESL	9	1	new	143	24					0.0013
GFLIIVLVM	9	1	new	193	24					<0.0002
IFSKASEYL	9	2		143	24					0.023
EYLQLVFGI	9	2		149	24					3.5
NWQYFFPVI	9	3		135	24					0.53
IFSKASSSL	9	3		143	24					0.016
LGSVVGNWQY	10	3		129	1	<0.0020		<0.0003	0.0012	
IFATCLGLSY	10	3		170	1	<0.0002		0.0005	0.0004	
TSCILESLFR	10	1	new	90	3			<0.0002	0.015	

Table 5

Sequence	AA	Mage Strain	Mol.	Pos.	Motif	A1	A2.1	A3.2	A11	A24
LESVIKNYKH	10	1	new	129	3			<0.0002	<0.0002	
REHSAYGEPR	10	1	new	227	3			<0.0002	<0.0002	
PDSDPARYEF	10	1	new	255	3			<0.0002	<0.0002	
LEYVIKVSAR	10	1	new	280	3			<0.0002	<0.0002	
VIKVSARVRF	10	1	new	283	3			<0.0002	<0.0002	
KVSARVRFFF	10	1	new	285	3			0.0013	0.0020	
STTINYTLWR	10	2		65	3			0.0014	0.091	
SSNQEEEGPR	10	2		80	3			<0.0002	<0.0002	
RMFPDLESEF	10	2		89	3			<0.0002	<0.0002	0.0016
ESEFQAAISR	10	2		95	3			<0.0002	<0.0002	
SEFQAAISRK	10	2		96	3			0.0012	0.0028	
ISRKMVELVH	10	2		102	3			<0.0002	<0.0002	
VELVHFLLLK	10	2		107	3			0.0009	0.0003	
ELVHFLLLKY	10	2,3		108	3			0.0066	0.0003	
LVHFLLLKYR	10	2		109	3			0.026	0.0022	
HFLLLKYRAR	10	2,3		111	3			0.0014	0.0002	
KAEMLESVLR	10	2		125	3			<0.0002	0.0009	
ESVLRNCQDF	10	2		130	3			<0.0002	<0.0002	
SVLRNCQDFF	10	2		131	3			<0.0002	<0.0002	
NCQDFFPVIF	10	2		135	3			<0.0002	<0.0002	
QDFFPVIFSK	10	2		137	3			<0.0002	0.0083	
PVIFSKASEY	10	2		141	3			0.016	0.0033	

Table 5

Sequence	AA	Mage Strain	Mol.	Pos.	Motif	A1	A2.1	A3.2	A11	A24
KASEYLQLVF	10	2		146	3			<0.0002	<0.0002	0.0030
EVVEVVPISH	10	2		158	3			<0.0002	<0.0002	
VEVVPISHLY	10	2		160	3			<0.0002	<0.0002	
ILVTCLGLSY	10	2		170	3			0.0036	0.0002	
LLGDNQVMPK	10	2		182	3			0.0093	0.0014	
IEGDCAPEEK	10	2		204	3			<0.0002	<0.0002	
STFPDLESEF	10	3		89	3			<0.0002	<0.0002	
ESEFQAALSR	10	3		95	3			<0.0002	<0.0002	
SEFQAALSRK	10	3		96	3			0.0010	0.0010	
LSRKVAELVH	10	3		102	3			<0.0002	<0.0002	
AELVHFLLLK	10	3		107	3			0.0008	<0.0002	
LVHFLLLKYR	10	3		109	3			0.040	0.0014	
GSVVGNWQYF	10	3		130	3			0.0020	0.0008	
SVVGNWQYFF	10	3		131	3			0.0085	0.0067	
KASSSLQLVF	10	3		146	3			0.0003	0.0008	0.0021
ELMEVDPIGH	10	3		158	3			<0.0003	<0.0002	
MEVDPIGHLY	10	3		160	3			0.0004	0.0004	
VDPIGHLYIF	10	3		162	3			<0.0003	<0.0002	
LIIVLAIIAR	10	3		195	3			0.028	0.0021	
REGDCAPEEK	10	3		204	3			<0.0003	<0.0002	
RQPSEGSSSR	10	1	new	74	11			0.0009	0.0009	
LQLVFGIDVK	10	1	new	151	11			0.0050	0.0018	

Table 5

Sequence	AA	Mage Strain	Mol.	Pos.	Motif	A1	A2.1	A3.2	A11	A24
RQVPDSDPAR	10	1	new	252	11			<0.0003	<0.0002	
MNYPLWSQSY	10	3	new	68	11			<0.0003	<0.0002	
GFLIIVLVMI	10	1	new	193	24					0.0008
SFSTTINYTL	10	2		63	24					0.015
EFQAAISRKM	10	2		97	24					<0.0002
LYILVTCLGL	10	2		168	24					0.014
NWQYFFPVIF	10	3		135	24					0.017
AVDPIGHLY	9	3	analog	161	1	8.0				
EADPIGHLY	9	3	analog	161	1	3.5				
EVDPASNTY	9	4		161	1	1.5				
EDTPIGHLY	9	3	analog	161	1	13				
EVDPTGHLY	9	3	analog	161	1	3.0				
AADSPSPPH	9	2		55	A11					
VPISHLYIL	9	2		170	P1					
MPKTGLLII	9	2		196	P1					
SMLEVFEGR	9	2		226	A11					
DSVFAHPRK	9	2		236	A11					
VFAHPRKLL	9	2		238	A24					
MQDLVQENY	9	2		247	A01					
DPACYEFLW	9	2		265	P2					
FLWGPRALI	9	2		271	A02					
ALIETSYVK	9	2		277	A03/A11					

Table 5

Sequence	AA	Mage Strain	Mol.	Pos.	Motif	A1	A2.1	A3.2	A11	A24
TSYVKVLHH	9	2		281	A11					
EPHISYPPL	9	2		296	P1					
ISYPPLHER	9	2		299	A03/A11					
YPPLHERAL	9	2		301	P1					
EPVTKAEML	9	2/3		128	P1					
VPGSDPACY	9	2/3		261	P2					
EGLEARGEA	9	3		14	A03					
GLEARGEAL	9	3		15	A02					
EARGEALGL	9	3		17	A02					
ALGLVGAQA	9	3		22	A02/A03					
GLVGAQAPA	9	3		24	A02/A03					
LVGAQAPAT	9	3		25	A02					
PATEEQEAA	9	3		31	A02/A03					
EAASSSSTL	9	3		37	A02					
AASSSSTLV	9	3		38	A02					
LVEVTLGEV	9	3		45	A02					
EVTLGEVPA	9	3		47	A02/A03					
VTLGEVPAA	9	3		48	A02/A03					
LPTTMNYPL	9	3		71	P1					
PDLESEFQA	9	3		99	A03					
HFLLLKYRA	9	3		118	A03					
FFPVIFSKA	9	3		146	A03					

Table 5

Sequence	AA	Mage Strain	Mol.	Pos.	Motif	A1	A2.1	A3.2	A11	A24
DPIGHLYIF	9	3		170	P2					
GDNQIMPKA	9	3		191	A03					
MPKAGLLII	9	3		196	P1					
AGLLIIVLA	9	3		199	A03					
KIWEELSVL	9	3		220	A02					
SVLEVFEGR	9	3		226	A03/A11					
EDSILGDPK	9	3		235	A03/A11					
SILGDPKKL	9	3		237	A02					
ILGDPKKLL	9	3		238	A02					
FLWGPRALV	9	3		271	A02					
PRALVETSY	9	3		275	A01					
RALVETSYV	9	3		276	A02					
ALVETSYVK	9	3		277	A03/A11					
LVETSYVKV	9	3		278	A02					
YVKVLHHMV	9	3		283	A02					
KVLHHMVKI	9	3		285	A02					
MVKISGGPH	9	3		290	A03/A11					
ISGGPHISY	9	3		293	A01/A03/A11					
GPHISYPPL	9	3		296	P1					
YPPLHEWVL	9	3		301	P1					
VPISHLYILV	10	2		170	P1					
MPKTGLLIIV	10	2		196	P1					

Table 5

Sequence	AA	Mage Strain	Mol.	Pos.	Motif	A1	A2.1	A3.2	A11	A24
VFEGREDSVF	10	2		230	A24					
HPRKLLMQDL	10	2		241	P1					
LMQDLVQENY	10	2		246	A01					
EFLWGPRALI	10	2		270	A24					
GPRALIETSY	10	2		274	P2					
RALIETSYVK	10	2		276	A11					
SYVKVLHHTL	10	2		282	A24					
SYPPLHERAL	10	2		300	A24					
APEEKIWEEL	10	2/3		216	P1					
PLEQRSQHCK	10	3		2	A03/A11					
HCKPEEGLEA	10	3		9	A03					
EARGEALGLV	10	3		17	A02					
RGEALGLVGA	10	3		19	A03					
EALGLVGAQA	10	3		21	A02/A03					
LGLVGAQAPA	10	3		23	A03					
GLVGAQAPAT	10	3		24	A02					
QAPATEEQEA	10	3		29	A02/A03					
EAASSSSTLV	10	3		37	A02					
TLVEVTLGEV	10	3		44	A02					
EVTLGEVPAA	10	3		47	A02/A03					
PDPPQSPQGA	10	3		59	A03					
LPTTMNYPLW	10	3		71	P2					

Table 5

Sequence	AA	Mage Strain	Mol.	Pos.	Motif	A1	A2.1	A3.2	A11	A24
PDLESEFQAA	10	3		99	A03					
YFFPVIFSKA	10	3		145	A03					
LGDNQIMPKA	10	3		190	A03					
MPKAGLLIIV	10	3		196	P1					
EVFEGREDSI	10	3		229	A02					
EDSILGDPKK	10	3		235	A03/A11					
SILGDPKKLL	10	3		237	A02					
ILGDPKKLLT	10	3		238	A02					
GDPKKLLTQH	10	3		240	A03/A11					
DPKKLLTQHF	10	3		241	P2					
LTQHFVQENY	10	3		246	A01/A03/A11					
FVQENYLEYR	10	3		250	A03/A11					
ACYEFLWGPR	10	3		267	A03/A11					
GPRALVETSY	10	3		274	P2					
RALVETSYVK	10	3		276	A03/A11					
ALVETSYVKV	10	3		277	A02					
LVETSYVKVL	10	3		278	A02					
YVKVLHHMVK	10	3		283	A03/A11					
MVKISGGPHI	10	3		290	A02					
KISGGPHISY	10	3		292	A01					
SPPHSPQGA	9	2		60	P2A					
APATEEQEA	9	3		30	P2A					

Table 5

Sequence	AA	Mage Strain	Mol.	Pos.	Motif	A1	A2.1	A3.2	A11	A24
DPPQSPQGA	9	3		60	P2A					
APATEEQQTA	10	2		30	P2A					
FPDLESEFQA	10	2/3		98	P2A					
APATEEQEAA	10	3		30	P2A					
DPIGHLYIFA	10	3		170	P2A					
EADPTGHSY	9	1		161	1	0.56	0	0	0.0002	<0.0002
KVADLVGFLL	10	1		105		0.0005	0.041	0.0039	0.0030	0.0070
ASSLPTTMNY	10	3		8	1	2.3			0.043	
TQDLVQEKY	9	1		240	1	0.57	0.0001	0	0	0
LVQEKYLEY	9	1		243	3	016	0	0.0016	0.0098	0
ILLWQPIPV	9	3				<0.0007	1.4	0.0048	0.0048	0
EVDPIGHLY	9	3				3.7			0.0022	
ASSFSTTINY	10	2		8	1	0.016	0	0.0016	0.0054	0
VTCLGLSY	8	1		172	1	0.022	0	0.0001	0.0007	0
SSLPTTMNY	9	3		9	1	0.037	0	0.013	0.12	0
GSVVGNWQY	9	3		77	1	0.0059	0	0.0009	0.025	0
DLVQEKYLEY	10	1	new	242	3	0	0	0.0010	0	0
SSFSTTINY	9	2		9	1	0.016	0	0.0095	0.056	0
MLESVIKNY	9	1		128	1	0.0016	0.0002	0.0006	0	0
KMVELVHFL	9	2				<0.0007	0.13	0.0007	0	0.0043
KMVELVHFLL	10	2		105		<0.0008	0.071	0.0004	0.0001	0.0008
LVFGIELMEV	10	3				0.0030	0.065	0.0007	0	0

Table 5

Sequence	AA	Mage Strain	Mol.	Pos.	Motif	A1	A2.1	A3.2	A11	A24
SLFRAVITK	9	1		96	3,11	<0.0007	0.0001	3.9	2.6	0
ADLVGFLLLK	10	1		107	3	0.0012	0.0003	0.0081	0.022	0
ESLFRAVITK	10	1		95	3	<0.0008	0	0.0090	0.0052	0
MLESVIKNYK	10	1				0	0	0.034	0.0045	0
LVGFLLLK	8	1		109	3	0.0029	0.0002	0.027	0.034	0
TTINFTRQR	9	1		66	3,11	0	0	0.051	0.40	0
LLGDNQIMPK	10	1/3		182	3,11	<0.0007	0.0001	0.022	0.016	0
SVMEVYDGR	9	1		219	3,11	<0.0006	0	0.059	0.32	0
HSAYGEPRK	9	1		229	3	0.0007	0	0.0070	0.0015	0
LLTQDLVQEK	10	1		238	3,11	<0.0007	0	0.0014	0.011	0
LTQDLVQEK	9	1		239	3,11	0.0011	0	0.0002	0.16	0
NYKHCFPEIF	10	1		135	24	0	0	0	0	0.26
LYIFATCLGL	10	3		115	24	<0.0007	0	0.0006	0	0.0035
NYPLWSQSY	9	3		16	24	<0.0006	0	0	0.0001	0.016
SYVLVTCL	8	1		168	24	0.0029	0.00025	0.0020	0.0002	0.0026
ETSYVKVLEY	10	1				0.075	0	0.0009	0.0004	0
TSYVKVLEY	9	1		275	3	0.082	0	0.23	0.013	0
FLWGPRALA	9	1				<0.0006	0.027	0.0015	0	0
ALAETSYVKV	10	1		271		<0.0007	0.017	0.0011	0.0029	0
RVRFFFPSLR	10	1		290	3	<0.0007	0	0.25	0.0035	0
ALAETSYVK	9	1				<0.0006	0.0002	0.17	0.39	0
LTQDLVQEKY	10	1		239	1	0.041	0	0	0.0002	0

Table 5

Sequence	AA	Mage Strain	Mol.	Pos.	Motif	A1	A2.1	A3.2	A11	A24
GFLLLKYRA	9	1						0.0004	0.0002	
CFPEIFGKA	9	1						0	0	
FFFPSLREA	9	1						0	0	
FFPSLREAA	9	1						0	0	
HCFPEIFGK	9	1		138	3,11			0.0017	0.0022	
RSLHCKPEEA	10	1						0.0001	0.0008	
EFLWGPRALA	10	1						0	0	
RFFFPSLREA	10	1						0.0004	0	
FFFPSLREAA	10	1						0	0	

Table 5

Sequence	Antigen	Strain	Molecule	Position	Motif	A1 Binding	A2 Binding	A3 Binding	A11 Binding	A24 Binding	Max. Binding
FSPAFDNLYY	c-ErbB2			1213	A01	5.5000		0.0005	0.0010		5.5000
CMQIAKGMSY	c-ErbB2			826	A01	0.2967		0.0003	0.0001		0.2967
ESMPNPEGRY	c-ErbB2			280	A01	0.1800		0.0003	0.0003		0.1800
ASCVTACPY	c-ErbB2			293	A01	0.0552		0.0008	0.0074		0.0552
FSPAFDNLY	c-ErbB2			1213	A01	0.0425		0.0002	0.0002		0.0425
ASPLDSTFY	c-ErbB2			997	A01	0.0290		0.0002	0.0004		0.0290
RGTQLFEDNY	c-ErbB2			103	A01	0.0205		0.0003	0.0015		0.0205
PASPLDSTFY	c-ErbB2			996	A01	0.0148		0.0003	0.0001		0.0148
LSAFSLHSY	HCV			2889	A01	0.8100		0.0002	0.0002		0.8100
KSTKVPAAY	HCV			1236	A01	0.0134		0.0009	0.0001		0.0134
DSSVLCECY	HCV			1513	A01	0.0110		0.0002	0.0003		0.0110
ETDPIGHLY	MAGE-3a	3	analog	161	A01	12.5000					12.5000
AVDPIGHLY	MAGE-3a	3	analog	161	A01	8.0000					8.0000
EVDPIAHLY	MAGE-3a	3	analog	161	A01	5.5000					5.5000
EVDAIGHLY	MAGE-3a	3	analog	161	A01	5.3500					5.3500
EVDPIGALY	MAGE-3a	3	analog	161	A01	5.0000					5.0000
EVDPIGHAY	MAGE-3a	3	analog	161	A01	4.6500					4.6500
EADPIGHLY	MAGE-3a	3	analog	161	A01	3.4500					3.4500
EVDPTGHLY	MAGE-3a	3	analog	161	A01	2.9500					2.9500
EVDPIGHSY	MAGE-3a	3	analog	161	A01	2.6667					2.6667
EVDPAGHLY	MAGE-3a	3	analog	161	A01	2.4000					2.4000
EVDPIGHLA	MAGE-3a	3	analog	161	A01	0.3300					0.3300
EVAPIGHLY	MAGE-3a	3	analog	161	A01	0.1800					0.1800
EVDPASNTY	MAGE-4	4		161	A01	1.5000					1.5000
VGSDCTTIHY	p53			225	A01	0.2600		0.0003	0.0003		0.2600
PSQKTYQGSY	p53			98	A01	0.0140		0.0003	0.0003		0.0140
PLSEDQLLY	PAP			147	A01	1.2000		0.0005	0.0001		1.2000
IPSYKKLIMY	PAP			277	A01	0.5650					0.5650
YASCHLTELY	PAP			310	A01	0.5467		0.0003	0.0002		0.5467

Table 5

Sequence	Antigen	Strain	Molecule	Position	Motif	A1 Binding	A2 Binding	A3 Binding	A11 Binding	A24 Binding	Max. Binding
RVLQGLPREY	c-ERB2			545	A03	0.0015		0.0350	0.0050		0.0350
QLVTQLMPY	c-ERB2			795	A03	0.0024		0.0112	0.0039		0.0112
VMAGVGSPY	c-ErbB2			773	A03	0.0400		0.0575	0.0079		0.0575
TLWKAGILY	HBV	adr	POL	724	A03	0.0017		0.2667	0.0016		0.2667
ILRGTSFVY	HBV	adr	POL	1345	A03	0.0017		0.0440	0.0002		0.0440
KLHWASQIY	HIV		POL	958	A03	0.0070		0.1160	0.0006		0.1160
GLNKIVRMY	HIV		GAG	274	A03	0.0017		0.0103	0.0002		0.0103
LVGFLLLKY	MAGE-1	1		109	A03	0.0033		0.0563	0.0012		0.0563
GTRVRAHAIY	p53			154	A03	0.0027		0.0365	0.0002		0.0365
KIQNFRVYY	HIV		POL	1474	A03/A11	0.0056		0.1190	0.1350		0.1350
SLYTKVVHY	PSA			237	A03/A11	0.0017		0.6750	0.0140		0.6750
LTCGFADIMGY	HCV			126	A11	2.4500		0.0003	0.0120	0.0001	2.4500
ETAYFLLK	HIV	con		1351	A11			0.0037	0.0425		0.0425
RWGLLLALL	c-ErbB2			8	A24					1.2567	1.2567
PYVSRLLGI	c-ErbB2			780	A24					0.1650	0.1650
VYMIMVKCW	c-ErbB2			951	A24					0.1640	0.1640
AYSLTLQGL	c-ErbB2			440	A24					0.1250	0.1250
SYGVTVWEL	c-ErbB2			907	A24					0.1200	0.1200
LYISAWPDSL	c-ErbB2			410	A24					0.0835	0.0835
VWSYGVTVW	c-ErbB2			905	A24					0.0800	0.0800
SYGVTVWELM	c-ErbB2			907	A24					0.0630	0.0630
TYLPTNASL	c-ErbB2			63	A24					0.0375	0.0375
VYMIMVKCWM	c-ErbB2			951	A24					0.0218	0.0218
RFRELVSEF	c-ErbB2			968	A24					0.0180	0.0180
CYGLGMEHL	c-ErbB2			342	A24					0.0176	0.0176
KWMALESIL	c-ErbB2			887	A24					0.0149	0.0149
EYLVPQQGFF	c-ErbB2			1022	A24					0.0120	0.0120
RYSEDPTVPL	c-ErbB2			1111	A24					0.0117	0.0117
RFTHQSDVW	c-ErbB2			898	A24					0.0107	0.0107

Table 5

Sequence	Antigen	Strain	Molecule	Position	Motif	A1 Binding	A2 Binding	A3 Binding	A11 Binding	A24 Binding	Max. Binding
EYLVSFGVWI	HBV		NUC	117	A24					0.0335	0.0335
WFHISCLTF	HBV		NUC	102	A24					0.0300	0.0300
QYLAGLSTL	HCV			1777	A24					0.0475	0.0475
TYSTYGKFL	HCV			1296	A24					0.0225	0.0225
QYSPGQRVEF	HCV			2614	A24					0.0175	0.0175
KFMLCAGRW	PSA			190	A24		0.0003			0.0305	0.0305

Table 6

AA	SEQUENCE	SOURCE
9	GLNKIVRMY	HIV GAG 274
9	KLNWASQIY	HIV POL 958
9	KIQNFRVYY	HIV POL 1474
9	TLWKAGILY	HBV adr POL 724
9	ILRGTSFVY	HBV adr POL 1345
9	SLYTKVVHY	PSA 237
9	NTSSSPQPK	p53 311
9	NVKIPVAIK	c-ERB2 745
10	TLGFGAYMSK	HCV LORF 1261
10	GTRVRAMAIY	p53 154
10	EAYSPVSTSK	HBV adw POL 887
9	QITKIQNFR	HIV POL 1471
9	NITGLILTR	HIV ENV 2633
9	FLWEWASVR	HBV adr ENV 324
9	RTPSPRRRR	HBV adr CORE 549
9	SLARGNQGR	HBV adr POL 805
10	VAYQATVCAR	HCV LORF 1587
10	KTYQGSYGFR	p53 101
9	WMCLRRFII	HBV ayw 237
9	WMCLRRFII	HBV ayw 237-245
9	KFMLCAGRW	PSA 190
10	IMPKTGFLII	MAGE 1 188
8	ETAYFLLK	HIV con 1351
11	LTCGFADIMGY	HCV 126
9	CSPHHTALR	HBV NUC;XNUCFUS 48
9	VMPKTGLLI	MAGE 2 188
9	VMPKTGLLI	MAGE2 188-196
9	VAELVHFLL	MAGE 3 106
9	IMPKAGLLI	MAGE 3 188
10	VMPKTGLLII	MAGE 2 188
10	VMPKTGLLII	MAGE2 188-197

AA	SEQUENCE	SOURCE
9	ASCVTACPY	c-ErbB2 293
9	VMAGVGSPY	c-ErbB2 773
9	ASPLDSTFY	c-ErbB2 997
9	FSPAFDNLY	c-ErbB2 1213
9	KSTKVPAAY	HCV 1236
9	DSSVLCECY	HCV 1513
9	LSAFSLHSY	HCV 2889
9	PLSEDQLLY	PAP 147
9	YAVCDKCLK	HPV 16 E6 67
9	CMSCCRSSR	HPV 16 E6 143
9	RWGLLLALL	c-ErbB2 8
9	TYLPTNASL	c-ErbB2 63
9	CYGLGMEHL	c-ErbB2 342
9	AYSLTLQGL	c-ErbB2 440
9	PYVSRLLGI	c-ErbB2 780
9	KWMALESIL	c-ErbB2 887
9	RFTHQSDVW	c-ErbB2 898
9	VWSYGVTVW	c-ErbB2 905
9	SYGVTVWEL	c-ErbB2 907
9	VYMIMVKCW	c-ErbB2 951
9	RFRELVSEF	c-ErbB2 968
9	WFHISCLTF	HBV NUC 102
9	TYSTYGKFL	HCV 1296
9	QYLAGLSTL	HCV 1777
10	IPSYKKLIMY	PAP 277
10	RGTQLFEDNY	c-ErbB2 103
10	ESMPNPEGRY	c-ErbB2 280
10	CMQIAKGMSY	c-ErbB2 826
10	PASPLDSTFY	c-ErbB2 996
10	FSPAFDNLYY	c-ErbB2 1213
10	PSQKTYQGSY	p53 98
10	VGSDCTTIHY	p53 225
10	YASCHLTELY	PAP 310
10	LYISAWPDSL	c-ErbB2 410

AA	SEQUENCE	SOURCE
10	SYGVTVWELM	c-ErbB2 907
10	VYMIMVKCWM	c-ErbB2 951
10	EYLVPQQGFF	c-ErbB2 1022
10	RYSEDPTVPL	c-ErbB2 1111
10	EYLVSFGVWI	HBV NUC 117
10	QYSPGQRVEF	HCV 2614
9	VYNFATCGI	LCMV glyco 35
9	GYCLTKWMI	LCMV glyco 283
9	MFEALPHII	LCMV glyco 7
9	IFALISFLL	LCMV glyco 43
9	LFKTTVNSL	LCMV glyco 342
9	LYTVKYPNL	LCMV nucleo 204
9	PYIACRTSI	LCMV nucleo 314
10	GYCLTKWMIL	LCMV glyco 283
10	AYLVSIFLHL	LCMV glyco 446
9	RWCIPWQRL	CEA 10
9	IYPNASLLI	CEA 101
9	LWWVNNQSL	CEA 177
9	LYGPDAPTI	CEA 234
9	VYAEPPKPF	CEA 318
9	LWWVNNQSL	CEA 355
9	LYGPDDPTI	CEA 412
9	TYYRPGVNL	CEA 425
9	LYGPDTPII	CEA 590
9	QYSWRINGI	CEA 624
9	TYACFVSNL	CEA 652
9	VWKTWGQYW	gp100 152
9	TWGQYWQFL	gp100 155
9	RYGSFSVTL	gp100 479
9	LMAVVLASL	gp100 606
9	HWLRLPRIF	gp100 636
9	SYKHEQVYI	PAP 96
9	AMTNLAALF	PAP 116
9	VFLTLSVTW	PSA 2

AA	SEQUENCE	SOURCE
9	TWIGAAPLI	PSA 9
9	CYASGWGSI	PSA 148
10	YMIMVKCWMI	c-ErbB2 952
10	RWCIPWQRLL	CEA 10
10	FWNPPTTAKL	CEA 27
10	QYSWFVNGTF	CEA 268
10	TFQQSTQELF	CEA 276
10	VYAEPPKPFI	CEA 318
10	YYRPGVNLSL	CEA 426
10	QYSWLIDGNI	CEA 446
10	SYLSGANLNL	CEA 604
10	HFLRNQPLTF	gp100 231
10	LFPPEGVSIW	PAP 123
10	TWIGAAPLIL	PSA 9
10	HYRKWIKDTI	PSA 244
9	KLRKPKHKK	P. falciparum CSP 104
9	KILSVFFLA	P. falciparum EXP-1 2
9	ALFFIIFNK	P. falciparum EXP-1 10
9	GTGSGVSSK	P. falciparum EXP-1 28
9	VLYNTEKGR	P. falciparum EXP-1 99
9	KYKLATSVL	P. falciparum EXP-1 73
9	PSENERGYY	P. falciparum LSA1 1664
9	FLKENKLNK	P. falciparum LSA1 111
9	GVSENIFLK	P. falciparum LSA1 105
9	ILVNLLIFH	P. falciparum LSA1 12
9	KSLYDEHIK	P. falciparum LSA1 1854

AA	SEQUENCE	SOURCE
9	LLIFHINGK	P. falciparum LSA1 16
9	QSSLPQDNR	P. falciparum LSA1 1676
9	QTNFKSLLR	P. falciparum LSA1 94
9	RINEEKHEK	P. falciparum LSA1 49
9	SLYDEHIKK	P. falciparum LSA1 1855
9	VLAEDLYGR	P. falciparum LSA1 1647
9	VLSHNSYEK	P. falciparum LSA1 60
9	FYFILVNLL	P. falciparum LSA1 9
9	YYIPHQSSL	P. falciparum LSA1 1671
9	PSDGKCNLY	P. falciparum TRAP 207
9	LACAGLAYK	P. falciparum TRAP 511
9	LLACAGLAY	P. falciparum TRAP 510
9	LSTNLPYGR	P. falciparum TRAP 122
9	QGINVAFNR	P. falciparum TRAP 192
9	RGDNFAVEK	P. falciparum TRAP 307
9	RSRKREILH	P. falciparum TRAP 262
9	SLLSTNLPY	P. falciparum TRAP 120
9	KYLVIVFLI	P. falciparum TRAP 8
9	PYAGEPAPF	P. falciparum TRAP 528

AA	SEQUENCE	SOURCE
10	VTCGNGIQVR	P. falciparum CSP 375
10	GTGSGVSSKK	P. falciparum EXP-1 28
10	LALFFIIFNK	P. falciparum EXP-1 9
10	FQDEENIGIY	P. falciparum LSA1 1794
10	FILVNLLIFH	P. falciparum LSA1 11
10	HVLSHNSYEK	P. falciparum LSA1 59
10	KSLYDEHIKK	P. falciparum LSA1 1854
10	ALLACAGLAY	P. falciparum TRAP 509
10	IIRLHSDASK	P. falciparum TRAP 100
10	LLACAGLAYK	P. falciparum TRAP 510
10	RLHSDASKNK	P. falciparum TRAP 102
9	ILGFVFTLT-NH2	Flu Matrix 59-67
10	KGILGFVFTL-NH2	Flu Matrix 57-66
9	KLQCVPLHV	PSA 166-174 P/D
9	KLQCVPLHV	PSA 166-174 P/D
9	KLQCVPLHV	PSA 166-174 P/D
11	KQVPLRPMTYK	940.03 N-terminal extension
9	KLYEIVAKV	A2.1 consensus
9	KLAEYVAKV	A2.1 consensus
9	KLAEIVYKV	A2.1 consensus
9	KVFEYLINK	A3.2 consensus
10	KVFPYALINK	A3.2 consensus
9	AVFAYAAAK	A3.2 consensus
9	ALEPAIAKY	A1 consensus

AA	SEQUENCE	SOURCE
9	YLEPAIAKY	A1 consensus
9	ALEPYIAKY	A1 consensus
9	YLEQYIEKY	A1 consensus
9	GTEKLLAKY	A1 consensus
9	ATEPAIAKY	A1 consensus
9	ATNYPAIQK	A11 consensus
9	ATNVPAIQK	A11 consensus
9	ATNAPYIQK	A11 consensus
9	ATNAVYIQK	A11 consensus
9	ATNAAYAQK	A11 consensus
9	AVNAAYAQK	A11 consensus
9	AVNAPYIQK	A11 consensus
9	AVNAVYIQK	A11 consensus
9	PTDPKLINY	A1 consensus
9	GTDPKLINY	A1 consensus
9	YTDPKLINF	A1 consensus
9	FTDPKLINY	A1 consensus
9	FTDQAVIKY	A1 consensus
9	YTDQAVIKF	A1 consensus
9	YTDQKLINF	A1 consensus
9	STNPKPQKK	HCV-core 2-10
11	STNPKPQKKNK	HCV-core 2-12
9	SFFPEITYI	self peptide of P815 analog; Y2 to F,
9	ATDPNFLLY	A1 consensus
9	ATDKNFLLY	A1 consensus
9	ALMEKIYQV	A2.1 consensus peptide
9	ALSEKIYQV	A2.1 consensus peptide
9	AVYDPIIQK	A3.2 consensus peptide
9	AVYDKIIQK	A3.2 consensus peptide
9	AVMNPMIQK	A11 consensus peptide

AA	SEQUENCE	SOURCE
9	AVMNEMIQK	A11 consensus peptide
9	AYMDMVNSF	A24 consensus peptide
9	AYIDNVNSF	A24 consensus peptide
9	KLAAAAAAK	A3.2/A11 poly-A analog
9	DVFRDPALK	Aw68 endogenous
9	GYKDGNEYI	Lm listeriolysin 91-99
10	MMWYWGPSLY	HBV
11	WMMWYWGPSLY	HBV
9	RYLRDQQLL	HIV env
8	FLLLKYRA	MAGE-1
9	IMPKTGFLI	MAGE-1
9	VADLVGFLL	MAGE-1
10	IMPKTGFLII	MAGE-1
11	FLIIVLVMIAM	MAGE-1
11	CILESCFRAVI	MAGE-1
9	MYRPDAIQL	P. Yoelii SSP2 143
10	NYSPNGNTNL	P. Yoelii SSP2 119
9	KFNPMKTHI	Kd consensus peptide
9	AMIKNLDFI	Db consensus
9	AMIKNLYFI	Db consensus analog
11	STLPETYVVRR	HCV 141-151 analog
9	QYDDAVYKL	Cw4 consensus
10	FQDPQERPRK	HPV16 E6
10	VFEFAFKDLF	HPV18 E6
9	VVYRDSIPH	HPV18 E6
9	IFEANGNLI	Flu HA 240-248
9	IYATVAGSL	HA 529-537

AA	SEQUENCE	SOURCE
9	SYIPSAEKI	P. bergaii CS 252-260
9	KYQAVTTTL	Tumour P198 14-22
10	MYPHFMPTNL	MCMV pp89 167-176
9	AYPNVSAKI	Lm listeriolysin 196-204
9	AYTGGKINI	Lm listeriolysin 413-421
9	SAISSILSK	HBV ENV 159
9	QAGFFLLTK	HBV ENV 190
9	SALYREALK	HBV NUC 64
9	RAKWNNTLK	HIV env 370
9	RATQIPSYK	PAP 273
9	TAAHCIRNK	PSA 58
9	MAVFIHNFK	HIV pol 909
9	TAGILELLK	HPV 6b E1 192
9	RAALLGKFK	HPV 6b E1 205
9	CATMCRHYK	HPV 6b E1 406
9	TAACSHEGK	Flu HA-1 132
9	NANANSAVK	P. fal csp 304
9	GAFKVPGVK	LCMV glyco 484
9	RARVHPTTR	HBV POL 244
9	CALPFTSAR	HBV X 69
9	NMLESILIK	LCMV nuc 259
9	WMILAAELK	LCMV glyco 289
9	EMNLPGRWK	HIV pol 107
9	SSLQSKHRK	HBV POL 201
9	GSTHVSWPK	HBV POL 398
9	TSDLEAYFK	HBV X NUC FUS 105
9	ASQIYAGIK	HIV pol 438
9	ASCDKCQLK	HIV pol 769
9	MSLAADLEK	LCMV nuc 100
9	VSSKNLMEK	Mel. tyro 25

AA	SEQUENCE	SOURCE
9	LSTNLPYGK	P. fal ssp2 122
9	STDHIPILY	A1 Nat. Processed
9	STAPPAHGV	Breast mucin 9-17
9	LMAVVLASL	gp100
9	WSQKRSFVY	gp100
9	PLDCVLYRY	gp100
10	PSSVGSRSEY	gp100
9	YTAVVPLVY	Hu J chain 102-110

Table 7

AA	SEQUENCE	SOURCE
8	LTELYFEK	PAP 315
9	TISPSYTYY	CEA 419
9	GTGCNGWFY	HPV 16/18 E1 11
9	LTEMVQWAY	HPV 6b/11 E1 358
9	ITVNNSGSY	CEA 289
9	CTGWFMVEA	HPV 6b/11 E1 14
9	ATVQDLKRK	HPV 6b/11 E1 77
9	AVESEISPR	HPV 6b/11 E1 101
9	FLNSNMQAK	HPV 6b/11 E1 393
9	ITRQTVIEH	HPV 6b/11 E1 341
9	IVGPPDTGK	HPV 6b/11 E1 476
9	KLIEPLSLY	HPV 6b/11 E1 254
9	KLWLHGTPK	HPV 6b/11 E1 462
9	KMSIKQWIK	HPV 6b/11 E1 420
9	VVAGFGIHH	HPV 6b/11 E1 238
9	HLFGYSWYK	CEA 61
9	ISPSYTYYR	CEA 420
9	HTQVLFIAK	CEA 636
9	ITVYAEPPK	CEA 316
9	ITVSAELPK	CEA 494
9	RLQLSNGNR	CEA 190
9	RLQLSNGNR	CEA 546
9	RINGIPQQH	CEA 628
9	SNMQAKYVK	HPV 6b/11 E1 396
9	EWITRQTVI	HPV 6b/11 E1 339
9	FFERLSSSL	HPV 6b/11 E1 613
9	NWKPIVQFL	HPV 6b/11 E1 439
10	PTISPSYTYY	CEA 418
10	PTISPLNTSY	CEA 240
10	HSASNPSPQY	CEA 616
10	KLIEPLSLYA	HPV 6b/11 E1 254
10	AIVGPPDTGK	HPV 6b/11 E1 475
10	DCATMCRHYK	HPV 6b/16 E1 405
10	KLWLHGTPKK	HPV 6b/11 E1 462
10	WVVAGFGIHH	HPV 6b/11 E1 237

AA	SEQUENCE	SOURCE
10	TITVSAELPK	CEA 493
10	TFWNPPTTAK	CEA 26
10	TISPSYTYYR	CEA 419
10	TISPLNTSYR	CEA 241
10	RTLTLFNVTR	CEA 198
10	RTLTLFNVTR	CEA 554
10	RTLTLLSVTR	CEA 376
10	ATPGPAYSGR	CEA 89
10	ASGHSRTTVK	CEA 483
10	QFLRHQNIEF	HPV 6b/11 E1 445
10	TFTFPNPFPF	HPV 6b/11 E1 586
9	RVDCTPLMY	Prost.Ca PSM 463
9	LLSLYGIHK	Prost.Ca PAP 243
9	SIVLPFDCR	Prost.Ca PSM 590
9	KSLYESWTK	Prost.Ca PSM 491
9	SMKHPQEMK	Prost.Ca PSM 615
9	SLYESWTKK	Prost.Ca PSM 492
9	YSLVHNLTK	Prost.Ca PSM 471
9	HLTELYFEK	Prost.Ca PAP 314
9	RATQIPSYK	Prost.Ca PAP 273
9	ASGRARYTK	Prost.Ca PSM 531
9	SLYGIHKQK	Prost.Ca PAP 245
9	RDYAVVLRK	Prost.Ca PSM 598
9	SSHDLMLLR	Prost.Ca PSA 113
9	GAAPLILSR	Prost.Ca PSA 12
9	KIVIARYGK	Prost.Ca PSM 199
9	RAAPLLLAR	Prost.Ca PAP 2
9	VVLRKYADK	Prost.Ca PSM 602
9	GLPDRPFYR	Prost.Ca PSM 680
9	WLDRSVLAK	Prost.Ca PAP 25
9	KVFRGNKVK	Prost.Ca PSM 207
9	IVRSFGTLK	Prost.Ca PSM 398
9	KIYSISMKH	Prost.Ca PSM 610
9	RSVLAKELK	Prost.Ca PAP 28
9	STNEVTRIY	Prost.Ca PSM 348
9	GFFLLGFLF	Prost.Ca PSM 31

AA	SEQUENCE	SOURCE
9	LYSDPADYF	Prost.Ca PSM 227
9	KYADKIYSI	Prost.Ca PSM 606
9	NYARTEDFF	Prost.Ca PSM 178
9	AYINADSSI	Prost.Ca PSM 448
9	SASFCGSPY	HBV POL 165
9	AFTFSPTYK	HBV POL 655
9	SVVRRAFPH	HBV POL 524
9	RWMCLRRFI	HBV ENV 236
9	SWLSLLVPF	HBV ENV 334
9	SWWTSLNFL	HBV ENV 197
9	PWTHKVGNF	HBV POL 51
9	SFCGSPYSW	HBV POL 167
10	NADSSIEGNY	Prost.Ca PSM 451
10	GLDSVELAHY	Prost.Ca PSM 104
10	RATQIPSYKK	Prost.Ca PAP 273
10	LGFLFGWFIK	Prost.Ca PSM 35
10	SSIEGNYTLR	Prost.Ca PSM 454
10	KSLYESWTKK	Prost.Ca PSM 491
10	SLLSLYGIHK	Prost.Ca PAP 242
10	FLYNFTQIPH	Prost.Ca PSM 73
10	VIYAPSSHNK	Prost.Ca PSM 690
10	AVVLRKYADK	Prost.Ca PSM 601
10	KSPDEGFEGK	Prost.Ca PSM 482
10	IVRSFGTLKK	Prost.Ca PSM 398
10	RIYNVIGTLR	Prost.Ca PSM 354
10	LSLYGIHKQK	Prost.Ca PAP 244
10	MSLLKNRFLR	Prost.Ca PSA 99
10	ISMKHPQEMK	Prost.Ca PSM 614
10	RAVCGGVLVH	Prost.Ca PSA 43
10	GSAPPDSSWR	Prost.Ca PSM 311
10	SIPVHPIGYY	Prost.Ca PSM 291
10	CSGKIVIARY	Prost.Ca PSM 196
10	ETYELVEKFY	Prost.Ca PSM 557
10	RLLQERGVAY	Prost.Ca PSM 440
10	FYDPMFKYHL	Prost.Ca PSM 565
10	TYSVSFDSLF	Prost.Ca PSM 624

AA	SEQUENCE	SOURCE
10	LYNFTQIPHL	Prost.Ca PSM 74
10	GWRPRRTILF	Prost.Ca PSM 409
10	FAAPFTQCGY	HBV POL 631
10	RWMCLRRFII	HBV ENV 236
10	WFVGLSPTVW	HBV ENV 345
10	SWPKFAVPNL	HBV POL 392
10	VFADATPTGW	HBV POL 686
9	FIFHKFQTK	HTLV-I tax 276
9	FLTNVPYKR	HTLV-I tax 182
9	ITWDPIDGR	HTLV-I tax 54
9	SALQFLIPR	HTLV-I tax 66
9	LSFPDPGLR	HTLV-I tax 131
9	QSSSFIFHK	HTLV-I tax 272
9	GLCSARLHR	HTLV-I tax 34
9	RLPSFPTQR	HTLV-I tax 74
9	AMRKYSPFR	HTLV-I tax 108
9	ISGGLCSAR	HTLV-I tax 31
9	ALFTAQEAK	HPV 16 E1 69
9	ATMCRHYKR	HPV 16 E1 406
9	FMSFLTALK	HPV 16 E1 453
9	GVSFSELVR	HPV 16 E1 216
9	KAAMLAKFK	HPV 16 E1 204
9	LTNILNVLK	HPV 16 E1 191
9	LVRPFKSNK	HPV 16 E1 222
9	MSFLTALKR	HPV 16 E1 454
9	NSNASAFLK	HPV 16 E1 386
9	QMSMSQWIK	HPV 16 E1 419
9	RLKAICIEK	HPV 16 E1 109
9	SLFGMSLMK	HPV 16 E1 484
9	SMSQWIKYR	HPV 16 E1 421
9	TAAALYWYK	HPV 16 E1 315
9	VVLLLVRYK	HPV 16 E1 274
9	ALLRYKCGK	HPV 18 E1 284
9	ATMCKHYRR	HPV 18 E1 413
9	CATMCKHYR	HPV 18 E1 412
9	FITFLGALK	HPV 18 E1 460

AA	SEQUENCE	SOURCE
9	GVLILALLR	HPV 18 E1 279
9	KLRAGQNHR	HPV 18 E1 647
9	LILALLRYK	HPV 18 E1 281
9	LTTNIHPAK	HPV 18 E1 571
9	NMSQWIRFR	HPV 18 E1 428
9	NSNAAAFLK	HPV 18 E1 393
9	SVAALYWYR	HPV 18 E1 322
9	WTYFDTYMR	HPV 18 E1 536
9	YVQAIVDKK	HPV 18 E1 19
9	IIKNFDIPK	GCDFP-15 36
9	VLAVQTELK	GCDFP-15 55
10	IIIKNFDIPK	GCDFP-15 35
10	TACLCDDNPK	GCDFP-15 87
10	AVLAVQTELK	GCDFP-15 54
10	TFYWDFYTNR	GCDFP-15 97
9	ASCHLTELY	PAP 311
10	KGEYFVEMYY	PAP 322
10	LTAAHCIRNK	PSA 57
9	PLYDMSLLK	PSA 95
9	QVHPQKVTK	PSA 182
9	SLLKNRFLR	PSA 100
9	YTKVVHYRK	PSA 239
9	TLWKAGILY	HBV pol 150
9	SLYTKVVHY	PSA 237
9	PVNRPIDWK	HBV POL 612
9	RHYLHTLWK	HBV POL 719
11	HTLWKAGILYK	HBV POL 149
11	GTDNSVVLSRK	HBV POL 735
11	RVTGGVFLVDK	HBV POL 357
8	ATQIPSYK	PAP 274
9	WMNSTGFTK	HCV consensus
9	RVLEDGVNY	HCV consensus
9	RLLAPITAY	HCV consensus
9	GVLAALAAY	HCV consensus
9	RVCEKMALY	HCV consensus

TABLE 8

PEPTIDE	AA	SEQUENCE
1235.01	10	AVFDRKSDAK
26.0149	9	CALRFTSAR
26.0153	9	SSAGPCALR
F104.02	9	SLTPPHSAK
F105.01	9	AIFQSSMTK
F105.02	9	GIFQSSMTK
F105.03	9	AAFQSSMTK
F105.04	9	AIAQSSMTK
F105.05	9	AIFASSMTK
F105.06	9	AIFQASMTK
F105.07	9	AIFQSAMTK
F105.08	9	AIFQSSATK
F105.09	9	AIFQSSMAK
F105.10	9	AIFQSSMTA
F105.11	9	FIFQSSMTK
F105.12	9	SIFQSSMTK
F105.14	9	ANFQSSMTK
F105.16	9	AIFQCSMTK
F105.17	9	AIFQSSMTR
F105.19	9	AIFQSSMTY
F105.20	9	AILQSSMTR
F105.21	9	AIFQRSMTR
F105.24	10	PAIFQSSMTK
F105.25	10	AIFQSSMTKI
27.0103	9	AIILHQQQK
27.0104	9	YGFRLGFLH
27.0108	9	SSCMGGMNR
27.0235	10	TCTYSPALNK
27.0239	10	NSSCMGGMNR
27.0240	10	SSCMGGMNRR
27.0250	10	KSKKGQSTSR
27.0252	10	TSRHKKLMFK
28.0062	8	FMFSPTYK
28.0063	8	FVFSPTYK
28.0066	8	TMLXMXXK

PEPTIDE	AA	SEQUENCE
28.0322	9	SMICSVVRR
28.0323	9	SVICSVVRR
28.0324	9	KVGNFTGLK
28.0325	9	KVGNFTGLR
28.0326	9	VVFFSQFSR
28.0327	9	SVNRPIDWK
28.0328	9	TLWKAGILK
28.0329	9	TLWKAGILR
28.0330	9	TMWKAGILY
28.0331	9	TVWKAGILY
28.0332	9	RMYLHTLWK
28.0333	9	RVYLHTLWK
28.0334	9	AMTFSPTYK
28.0335	9	AVTFSPTYK
28.0336	9	SVVRRAFPR
28.0337	9	SVVRRAFPK
28.0338	9	ISEYRHYXY
28.0339	9	GTGXNGWFY
28.0340	9	ASXHLTELY
28.0341	9	ASXDKXQLK
28.0371	9	RVXEKMALY
28.0372	9	XTGWFMVEA
28.0374	9	HISXLTFGR
28.0375	9	AVXTRGVAK
28.0377	9	HLIFXHSKK
28.0378	9	HTMLXMXXK
28.0381	9	RLKAIXIEK
28.0383	9	TLFXASDAK
28.0384	9	ALLRYKXGK
28.0387	9	ATMXRHYKR
28.0388	9	XATMXRHYK
28.0390	9	ATMXKHYRR
28.0391	9	LLAXAGLAY
28.0392	9	LAXAGLAYK
28.0393	9	SIVLPFDXR
28.0394	9	AAXWWAGIK
28.0628	10	QMFTFSPTYK

PEPTIDE	AA	SEQUENCE
28.0629	10	QVFTFSPTYK
28.0630	10	TMWKAGILYK
28.0631	10	TVWKAGILYK
28.0632	10	VMGGVFLVDK
28.0633	10	VVGGVFLVDK
28.0635	10	SVLPETTVVR
28.0638	10	HTLWKAGILK
28.0640	10	HMLWKAGILY
28.0395	9	SAIXSVVRR
28.0644	10	GTFNSVVLSR
28.0645	10	YMFDVVLGAK
28.0646	10	MMWYWGPSLK
28.0647	10	MMWYWGPSLR
28.0665	10	IVGGWEXEK
28.0667	10	IILEXVYXK
28.0668	10	SIPHAAXHK
28.0670	10	IVXPIXSQK
28.0671	10	LIRXLRXQK
28.0672	10	XTYSPALNK
28.0675	10	TVXAGGXAR
28.0676	10	HISXLTFGR
28.0677	10	XVNXSQFLR
28.0678	10	LIFXHSKKK
28.0679	10	FVLGGXRHK
28.0713	10	TSAIXSVVRR
28.0714	10	HLIFXHSKKK
28.0715	10	LLIRXINXQK
28.0716	10	GIVXPIXSQK
28.0717	10	LLIRXLRXQK
28.0718	10	SLEQRSLHXK
28.0720	10	RIVGGWEXEK
28.0721	10	DIILEXVYXK
28.0722	10	XVYXKQQLLR
28.0723	10	RAVXGGVLVH
28.0725	10	LTAAHXIRNK
28.0728	10	KAAXWWAGIK
28.0730	10	VVRRXPHHER

PEPTIDE	AA	SEQUENCE
28.0731	10	LLGIWGXSGK
28.0732	10	TTLFXASDAK
28.0734	10	RTVXAGGXAR
28.0736	10	GTQRXEKXSK
28.0737	10	LVQNANPDXK
28.0738	10	VTXGNGIQVR
28.0739	10	DXATMXRHYK
28.0740	10	GLAXHQLXAR
28.0741	10	ALLAXAGLAY
28.0742	10	LLAXAGLAYK
28.0743	10	XVARXPSGVK
28.0745	10	LVEIXTEMEK
28.0746	10	LLNWXMQIAK
28.0824	11	HMLWKAGILYK
28.0825	11	HVLWKAGILYK
28.0826	11	SMLPETTVVRR
28.0827	11	SVLPETTVVRR
28.0828	11	GMDNSVVLSRK
28.0829	11	GVDNSVVLSRK
28.0830	11	GTFNSVVLSRK
28.0369	9	GLAXHQLXA
1259.02	9	DTVDTVLEK
1259.10	9	PVTIGECPK
1259.14	10	FTAVGKEFNK
1259.16	11	RTLDFHDSNVK
1259.21	11	KTRPILSPLTK
1259.26	11	GTHPSSSAGLK
1259.28	11	ILWILDRLFFK
1259.29	9	WILDRLFFK
1259.30	11	CIYRRFKYGLK
1259.31	9	KSMREEYRK
1259.33	9	YIQMCTELK
1259.37	10	MVMELVRMIK
1259.38	9	VMELVRMIK
1259.41	11	LIRPNENPAHK
26.0023	8	VSFGVWIR
26.0024	8	VSIPWTHK

PEPTIDE	AA	SEQUENCE
26.0026	8	ASFCGSPY
26.0035	9	TSPYELSLY
26.0036	9	TSIPFLHEY
26.0041	9	FNDPGPGTY
26.0045	9	YVDLGALRY
26.0051	9	DADRSFIEY
26.0055	9	NMDKAVKLY
26.0056	9	TTDNFYRNY
26.0058	9	HSAEALQKY
26.0059	9	LTAGLDFAY
26.0061	9	LTYKYNQFY
26.0062	9	CSNDKSLVY
26.0063	9	RSARASSRY
26.0065	9	ASADKPYSY
26.0067	9	STTAGPNEY
26.0069	9	LSGNGHFHY
26.0073	9	NTFVQANLY
26.0074	9	GTATYLPPY
26.0081	9	RLDAFRQTY
26.0082	9	KAEVHTFYY
26.0083	9	VAEGDTVIY
26.0084	9	LTEIDIRDY
26.0085	9	HTEFEGQVY
26.0086	9	VSDGGPNLY
26.0092	9	IIEDQYNRY
26.0093	9	FLDQWWTEY
26.0095	9	FVEDPNGKY
26.0096	9	ISDESYRVY
26.0156	9	YLAEADLSY
26.0197	9	ALLAVGATK
26.0198	9	ALNFPGSQK
26.0199	9	AVGATKVPR
26.0203	9	FSVSVSQLR
26.0204	9	GTATLRLVK
26.0205	9	GVSRQLRTK
26.0207	9	LIYRRRLMK
26.0211	9	QLVLHQILK

PEPTIDE	AA	SEQUENCE
26.0212	9	SSHWLRLPR
26.0214	9	TMEVTVYHR
26.0216	9	VLASLIYRR
26.0217	9	VSCQGGLPK
26.0218	9	VVLASLIYR
26.0227	9	GTQCALTRR
26.0251	9	FTIPYWDWR
26.0252	9	GTPEGPLRR
26.0253	9	KSYLEQASR
26.0255	9	LVSLLCRHK
26.0256	9	MVPFIPLYR
26.0258	9	QTSAGHFPR
26.0259	9	SIFEQWLRR
26.0260	9	SLLCRHKRK
26.0261	9	SSWQIVCSR
26.0267	10	NMQIGGVLTY
26.0273	10	RMAQNFAMRY
26.0274	10	FTVQGSLSGY
26.0275	10	QTSPYELSLY
26.0276	10	SSNAILSLSY
26.0280	10	TSQPWWPADY
26.0284	10	VSDVSIIIPY
26.0285	10	ASDAQSANKY
26.0286	10	FTETNLAGEY
26.0287	10	YVDGFEPNGY
26.0291	10	FNDPGPGTYY
26.0296	10	FLDQWWTEYY
26.0299	10	AAEFATETAY
26.0309	10	NAEVVLNQLY
26.0311	10	FVDGDSLFEY
26.0316	10	PSEDAQVAVY
26.0317	10	MSDNIRTGLY
26.0318	10	ESELREILNY
26.0319	10	CMESVRNGTY
26.0320	10	KTENGITRLY
26.0321	10	LTEIDIRDYY
26.0397	10	LLVLMAVVLA

PEPTIDE	AA	SEQUENCE
26.0424	10	AVVLASLIYR
26.0425	10	GALLAVGATK
26.0426	10	GTATLRLVKR
26.0427	10	HTMEVTVYHR
26.0428	10	IALNFPGSQK
26.0432	10	QLRALDGGNK
26.0433	10	QVPLDCVLYR
26.0434	10	SLIYRRRLMK
26.0435	10	SSSHWLRLPR
26.0438	10	TVSCQGGLPK
26.0442	10	VVLASLIYRR
26.0466	10	YVKVLHHTLK
26.0473	10	LIGCWYCRRR
26.0474	10	LLIGCWYCRR
26.0485	10	SSMHNALHIY
26.0504	10	CVSSKNLMEK
26.0510	10	FSSWQIVCSR
26.0511	10	GLVSLLCRHK
26.0518	10	YMVPFIPLYR
26.0535	11	GVWIRTPPAYR
26.0539	11	RLVVDFSQFSR
26.0545	11	TLPETTVVRRR
26.0549	11	LLPIFFCLWVY
	11	STLPETTVVRR
26.0550	11	RAFPHCLAFSY

Table 9

Sequence	AA	Mage strain	Mol.	Pos.	Motif	A1	A2.1	A3.2	A11	A24
ALEAQQEAL	9	1		15	2.1		<0.0003			
ILESLFRAV	9	1		93	2.1		0.0004			
VITKKVADL	9	1		101	2.1		<0.0003			
CLGLSYDGL	9	1/3		174	2.1		0.0004			
QIMPKTGFL	9	1		187	2.1		0.0007			
SLHCKPEEAL	10	1		7	2.1		0.0002			
PLVLGTLEEV	10	1		37	2.1		0.0008			
CILESLFRAV	10	1		92	2.1		0.0003			
AVITKKVADL	10	1		100	2.1		0			
VITKKVADLV	10	1		101	2.1		0			
LLKYRAREPV	10	1/3		114	2.1		0			
EIFGKASESL	10	1		142	2.1		0			
CLGLSYDGLL	10	1/3		174	2.1		0			
AISRKMVEL	9	2		101	2.1		0.0003			
KMVELVHFL	9	2		105	2.1		0.16			
MVELVHFLL	9	2		106	2.1		0.0031			
DLQQSLRVL	9	2		143	2.1		0			
SLRVLAAGL	9	2		147	2.1		0.0001			
ALSRKVAEL	9	3		101	2.1		0.0050			
HLYIFATCL	9	3		167	2.1		0.0003			
YIFATCLGL	9	3		169	2.1		0.018			
QIMPKAGLL	9	3		187	2.1		0			

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Sequence	AA	Mage Strain	Mol.	Pos.	Motif	A1	A2.1	A3.2	A11	A24
AISRKMVELV	10	2		101	2.1		0			
MVELVHFLLL	10	2		106	2.1		0.0017			
KLPGLLSRDL	10	2		135	2.1		0			
LLSRDLQQSL	10	2		139	2.1		0.0007			
SLPTTMNYPL	10	3		63	2.1		0.0035			
DLESEFQAAL	10	3		93	2.1		0.0001			
ALSRKVAELV	10	3		101	2.1		0.0001			
KVAELVHFLL	10	3		105	2.1		0.012			
VIFSKASSSL	10	3		142	2.1		0			
SLQLVFGIEL	10	3		150	2.1		0.0049			
LMEVDPIGHL	10	3		159	2.1		0.0005			
FLIIVLVMI	9	1		194	2.1		0.0005			
GLLGDNQIM	9	1		181	2.1		0.0051			
SLHCKPEEA	9	1		7	2.1		0.013	<0.0002	0	
ALGLVCVQA	9	1		22	2.1		0.015	<0.0002	<0.0002	
CKPEEALEA	9	1		10	Random		<0.0002			
QQEALGLVC	9	1		19	Random		<0.0002			
VQAATSSSS	9	1		28	Random		<0.0002			
PLVLGTLEE	9	1		37	Random		<0.0002			
VPTAGSTDP	9	1		46	Random		<0.0002			
PQSPQGASA	9	1		55	Random		<0.0002			
FPTTINFTR	9	1		64	Random		<0.0002			

Sequence	AA	Mage Strain	Mol.	Pos.	Motif	A1	A2.1	A3.2	A11	A24
QRQPSEGSS	9	1		73	Random		<0.0002			
SREEEGPST	9	1		82	Random		<0.0002			
AVITKKVAD	9	1		100	Random		<0.0002			
EMLESVIKN	9	1		127	Random		<0.0002			0
YKHCFPEIF	9	1		136	Random		<0.0002			
GKASESLQL	9	1		145	Random		<0.0002			
VFGIDVKEA	9	1		154	Random		<0.0002	<0.0002	0	
DPTGHSYVL	9	1		163	Random		<0.0002			
VTCLGLSYD	9	1		172	Random		<0.0002			
PKTGFLIIV	9	1		190	Random		<0.0002			
LVMIAMEGG	9	1		199	Random		<0.0002			
HAPEEEIWE	9	1		208	Random		<0.0002			
ELSVMEVYD	9	1		217	Random		<0.0002			
GREHSAYGE	9	1		226	Random		<0.0002			
PRKLLTQDL	9	1		235	Random		0.0002			
VQEKYLEYG	9	1		244	Random		<0.0002			
RCRTVIPHA	9	1		253	Random		<0.0002			
MSSCGVQGP	9	1		262	Random		<0.0002			
ILESLFRAVI	10	1		93	2.1		0.0002			
FLIIVLVMIA	10	1		194	2.1		0.0003	0.0093	0.0030	
LVFGIDVKEA	10	1		153	2.1		0.0002	<0.0002	0	
EVYDGREHSA	10	1		222	2.1		0	<0.0002	0	

Sequence	AA	Mage Strain	Mol.	Pos.	Motif	A1	A2.1	A3.2	A11	A24
GVQGPSLKPA	10	1		266	2.1		0.0001			
QLVFGIDV	8	1		152	2.1		0			
KLLTQDLV	8	1		237	2.1		0.0004			
GLLGDNQI	8	1		181	2.1		0			
DLVGFLLL	8	1		108	2.1		0			
GLSYDGLL	8	1		176	2.1		0.0001			
DLVQEKYL	8	1		242	2.1		0			
LLGDNQIM	8	1		182	2.1		0			
FLIIVLVM	8	1		194	2.1		0			
ALEAQQEA	8	1		15	2.1		0			
TLEEVPTA	8	1		42	2.1		0			
IMPKTGFL	8	1		188	2.1		0.0001			
PVTKAEML	8	1		122	2.1		0			
IVLVMIAM	8	1		197	2.1		0.0001			
AVITKKVA	8	1		100	2.1		0			
EIWEELSV	8	1		213	2.1		0			
LIIVLVMI	8	1		195	2.1		0.0001			
IIVLVMIA	8	1		196	2.1		0.0002			
SLFRAVITKKV	11	1		96	2.1		0.0001			
LLLKYRAREPV	11	1		113	2.1		0.0001			
YLEYGRCRTVI	11	1		248	2.1		0.0006			
ALEAQQEALGL	11	1		15	2.1		0.0001			

Sequence	AA	Mage Strain	Mol.	Pos.	Motif	A1	A2.1	A3.2	A11	A24
FLIIVLVMIAM	11	1		194	2.1		0.0041			
VLGTLEEVPTA	11	1		39	2.1		0.0002			
QLVFGIDVKEA	11	1		152	2.1		0.0001			
AVITKKVADLV	11	1		100	2.1		0			
PVTKAEMLESV	11	1		122	2.1		0			
KVADLVGFLLL	11	1		105	2.1		0.020			
GVQGPSLKPAM	11	1		266	2.1		0			
LVGFLLLKYRA	11	1		109	2.1		0.0004			
LVMIAMEGGHA	11	1		199	2.1		0.0005			
CILESLFRAVI	11	1		92	2.1		0.0030			
EALEAQQEA	9	1		14	2.1		0	<0.0002	0	
EAQQEALGL	9	1		17	2.1		0			<0.0002
AATSSSSPL	9	1		30	2.1		0			<0.0002
ATSSSSPLV	9	1		31	2.1		0.0007			
GTLEEVPTA	9	1		41	2.1		0.013	<0.0002	0	
GASAFPTTI	9	1		60	2.1		0			<0.0002
STSCILESL	9	1		89	2.1		0.0002			
RAVITKKVA	9	1		99	2.1		0	<0.0002	0	
ITKKVADLV	9	1		102	2.1		0			
RAREPVTKA	9	1		118	2.1		0			
KAEMLESVI	9	1		125	2.1		0			<0.0002
KASESLQLV	9	1		146	2.1		0.0009			

Sequence	AA	Mage Strain	Mol.	Pos.	Motif	A1	A2.1	A3.2	A11	A24
PTGHSYVLV	9	1		164	2.1		0			
KTGFLIIVL	9	1		191	2.1		0.0006			
LIIVLVMIA	9	1		195	2.1		0	0.0022	0.0006	
IIVLVMIAM	9	1		196	2.1		0.0007			
MIAMEGGHA	9	1		201	2.1		0.0005	<0.0002	0.0002	
EIWEELSVM	9	1		213	2.1		0			
SAYGEPRKL	9	1		230	2.1		0.0002			<0.0002
YLEYGRCRT	9	1		248	2.1		0			
EALGLVCVQA	10	1		21	2.1		0.0005	<0.0002	0	
QAATSSSSPL	10	1		29	2.1		0			<0.0002
VTKAEMLESV	10	1		123	2.1		0			
EADPTGHSYV	10	1		161	2.1		0			
VLGTLEEVPT	10	1		39	2.1		0.0004			
SAFPTTINFT	10	1		62	2.1		0			
GIDVKEADPT	10	1		156	2.1		0			
PTGHSYVLVT	10	1		164	2.1		0			
FLWGPRALA	9	1	new	265	2.1		0.042	0.0017	0	
LAETSYVKV	9	1	new	272	2.1		0			
YVKVLEYVI	9	1	new	277	2.1		0.0002			
RVRFFFPSL	9	1	new	290	2.1		0.0001			
LAETSYVKVL	10	1	new	272	2.1		0			<0.0002
VLEYVIKVSA	10	1	new	280	2.1		0.0002	0.0002	0	

Sequence	AA	Mage Strain	Mol.	Pos.	Motif	A1	A2.1	A3.2	A11	A24
AALREEEEGV	10	1	new	301	2.1		0			
SMHCKPEEV	9	1	new (a)	7	2.1		0.018			
AMGLVCVQV	9	1	new (a)	22	2.1		0.012			
LMLGTLEEV	9	1	new (a)	38	2.1		0.13			
LQLVFGIDV	9	1	new	151	2.1		0.0004			
GLSYDGLLG	9	1	new	176	2.1		0			
GLSYDGLLV	9	1	new (a)	176	2.1		0.0047			
LLGDNQIMP	9	1	new	182	2.1		0.0001			
LLGDNQIMV	9	1	new (a)	182	2.1		0.043			
WEELSVMEV	9	1	new	215	2.1		0			
WMELSVMEV	9	1	new (a)	215	2.1		0.041			
RKLLTQDLV	9	1	new	236	2.1		0			
YEFLWGPRA	9	1	new	262	2.1		0			
YMFLWGPRV	9	1	new (a)	262	2.1		0.22			
AATSSSSPLV	10	1	new	30	2.1		0			
ATSSSSPLVL	10	1	new	31	2.1		0			
KMADLVGFLV	10	1	new (a)	105	2.1		1.5			
VADLVGFLLL	10	1	new	106	2.1		0.0008			0.0003
SESLQLVFGI	10	1	new	148	2.1		0			
VMVTCLGLSV	10	1	new (a)	170	2.1		0.30			
QIMPKTGFLI	10	1	new	187	2.1		0.0009			
QMMPKTGFLV	10	1	new (a)	187	2.1		0.050			

Sequence	AA	Mage Strain	Mol.	Pos.	Motif	A1	A2.1	A3.2	A11	A24
KTGFLIIVLV	10	1	new	191	2.1		0.0012			
LIIVLVMIAM	10	1	new	195	2.1		0.0003			
VMIAMEGGHV	10	1	new (a)	200	2.1		0.053			
SAYGEPRKLL	10	1	new	230	2.1		0			0.0008
ALAETSYVKVL	11	1 N		270	2.1		0.012			
KMVELVHFLLL	11	2		52	2.1		0.67			
ELMEVDPIGHL	11	3		105	2.1		0.026			
HLYIFATCLGL	11	3		114	2.1		0.041			
LLLKYRAREPV	11	3		60	2.1		0.0001			
QLVFGIELMEV	11	3		99	2.1		0.34			
IMPKAGLLIIV	11	3		135	2.1		0.013			
VLVTCLGLSYDGL	13	1 n	E6	170	2.1		0.0017			
KLLTQDLVQEKYL	13	1 n	E6	237	2.1		0.0060			
DLVQEKYLEYRQV	13	1 n	E6	242	2.1		0			
SLFRAVITKKVADLV	15	1 n	POL	96	2.1		0.0004			
DLESEFQAAISRKMV	15	2	POL	40	2.1		0			
MLGSVVGNWQYFFPV	15	3	POL	75	2.1		0.012			
GASSFSTTI	9	2		60	2.1		0			0.0002
DLESEFQAA	9	2,3		93	2.1		0			
QAAISRKMV	9	2		99	2.1		0			
KAEMLESVL	9	2		125	2.1		0			0
KASEYLQLV	9	2		146	2.1		0.011			

Sequence	AA	Mage Strain	Mol.	Pos.	Motif	A1	A2.1	A3.2	A11	A24
QLVFGIEVV	9	2		152	2.1		0.0038			
VVPISHLYI	9	2		162	2.1		0.0002			
PISHLYILV	9	2		164	2.1		0.0005			
HLYILVTCL	9	2		167	2.1		0.0034			
YILVTCLGL	9	2		169	2.1		0.0014			
GLLGDNQVM	9	2		181	2.1		0.0038			
QVMPKTGLL	9	2		187	2.1		0			
VMPKTGLLI	9	2		188	2.1		0.0010			0.230
KTGLLIIVL	9	2		191	2.1		0.0002			
GLLIIVLAI	9	2,3		193	2.1		0.0002			
LLIIVLAII	9	2,3		194	2.1		0.0001			
LIIVLAIIA	9	2,3		195	2.1		0.0008			
IIVLAIIAI	9	2		196	2.1		0.0009			
IIAIEGDCA	9	2		201	2.1		0			
GASSLPTTM	9	3		60	2.1		0			0.0010
QAALSRKVA	9	3		99	2.1		0			
VAELVHFLL	9	3		106	2.1		0			0.039
KAEMLGSVV	9	3		125	2.1		0			
KASSSLQLV	9	3		146	2.1		0.0005			
QLVFGIELM	9	3		152	2.1		0.0010			
PIGHLYIFA	9	3		164	2.1		0			
IMPKAGLLI	9	3		188	2.1		0.0064			

Sequence	AA	Mage Strain	Mol.	Pos.	Motif	A1	A2.1	A3.2	A11	A24
KAGLLIIVL	9	3		191	2.1		0.0002			0
IIAREGDCA	9	3		201	2.1		0			
EALEAQQEAL	10	1	new	14	2.1		0			0
EAQQEALGLV	10	1	new	17	2.1		0			
DLESEFQAAI	10	2		93	2.1		0			
AAISRKMVEL	10	2		100	2.1		0			0
VIFSKASEYL	10	2		142	2.1		0.0014			
YLQLVFGIEV	10	2		150	2.1		0.37			
LVFGIEVVEV	10	2		153	2.1		0.012			
GIEVVEVVPI	10	2		156	2.1		<0.0002			
VVEVVPISHL	10	2		159	2.1		<0.0002			
EVVPISHLYI	10	2		161	2.1		<0.0002			
VVPISHLYIL	10	2		162	2.1		0.0002			
PISHLYILVT	10	2		164	2.1		0.0003			
QVMPKTGLLI	10	2		187	2.1		0.0002			
VMPKTGLLII	10	2		188	2.1		0.0009			0.058
KTGLLIIVLA	10	2		191	2.1		<0.0002			
GLLIIVLAII	10	2,3		193	2.1		0.0005			
LLIIVLAIIA	10	2,3		194	2.1		<0.0002			
LIIVLAIIAI	10	2		195	2.1		0.0013			
AIIAIEGDCA	10	2		200	2.1		0.0023			
AALSRKVAEL	10	3		100	2.1		0.0007			0

Sequence	AA	Mage Strain	Mol.	Pos.	Motif	A1	A2.1	A3.2	A11	A24
VAELVHFLLL	10	3		106	2.1		0.0009			0.0018
VTKAEMLGSV	10	3		123	2.1		<0.0002			
GIELMEVDPI	10	3		156	2.1		<0.0002			
EVDPIGHLYI	10	3		161	2.1		<0.0002			
PIGHLYIFAT	10	3		164	2.1		0.0003			
QIMPKAGLLI	10	3		187	2.1		0.0006			
IMPKAGLLII	10	3		188	2.1		0.0015			
KAGLLIIVLA	10	3		191	2.1		<0.0002			
AIIAREGDCA	10	3		200	2.1		<0.0002			
FLWGPRALI	9	2		271	A02					
GLEARGEAL	9	3		15	A02					
EARGEALGL	9	3		17	A02					
ALGLVGAQA	9	3		22	A02/A03					
GLVGAQAPA	9	3		24	A02/A03					
LVGAQAPAT	9	3		25	A02					
PATEEQEAA	9	3		31	A02/A03					
EAASSSSTL	9	3		37	A02					
AASSSSTLV	9	3		38	A02					
LVEVTLGEV	9	3		45	A02					
EVTLGEVPA	9	3		47	A02/A03					
VTLGEVPAA	9	3		48	A02/A03					
KIWEELSVL	9	3		220	A02					

Sequence	AA	Mage Strain	Mol.	Pos.	Motif	A1	A2.1	A3.2	A11	A24
SILGDPKKL	9	3		237	A02					
ILGDPKKLL	9	3		238	A02					
FLWGPRALV	9	3		271	A02					
RALVETSYV	9	3		276	A02					
LVETSYVKV	9	3		278	A02					
YVKVLHHMV	9	3		283	A02					
KVLHHMVKI	9	3		285	A02					
EARGEALGLV	10	3		17	A02					
EALGLVGAQA	10	3		21	A02/A03					
GLVGAQAPAT	10	3		24	A02					
QAPATEEQEA	10	3		29	A02/A03					
EAASSSSTLV	10	3		37	A02					
TLVEVTLGEV	10	3		44	A02					
EVTLGEVPAA	10	3		47	A02/A03					
EVFEGREDSI	10	3		229	A02					
SILGDPKKLL	10	3		237	A02					
ILGDPKKLLT	10	3		238	A02					
ALVETSYVKV	10	3		277	A02					
LVETSYVKVL	10	3		278	A02					
MVKISGGPHI	10	3		290	A02					
LVLGTLEEV	9	1		38	2.1	<0.0006	0.032	0	0	0.0003
KVADLVGFLL	10	1		105		0.0005	0.041	0.0039	0.0030	0.0070

Sequence	AA	Mage Strain	Mol.	Pos.	Motif	A1	A2.1	A3.2	A11	A24
LVFGIELMEV	10	3		153	2.1		0.17			
ILLWQPIPV	9	3				<0.0007	1.4	0.0048	0.0048	0
EVDPIGHLY	9	3				3.7			0.0022	
KMVELVHFL	9	2				<0.0007	0.13	0.0007	0	0.0043
KMVELVHFLL	10	2		105		<0.0008	0.071	0.0004	0.0001	0.0008
LVFGIELMEV	10	3				0.0030	0.065	0.0007	0	0
KVAELVHFL	9	3		105	2.1	0	0.073	0.011	0.0047	0.0005
CILESLFRA	9	1		92	2.1	0.0001	0.073	0	0.0002	0
VMIAMEGGHA	10	1		200	2.1	<0.00008	0.0023	0	0	0
MLESVIKNYK	10	1				0	0	0.034	0.0045	0
ETSYVKVLEY	10	1				0.075	0	0.0009	0.0004	0
KVLEYVIKV	9	1	new	279	2.1	<0.0005	0.095	0.022	0.015	0
FLWGPRALA	9	1				<0.0006	0.027	0.0015	0	0
ALREEEEGV	9	1		302	2.1	<0.0006	0.0056	0	0	0
ALAETSYVKV	10	1		271		<0.0007	0.017	0.0011	0.0029	0
YVIKVSARV	9	1		283	2.1	0.0005	0.018	0	0	0
RALAETSYV	9	1		270	2.1	<0.0006	0.014	0.0003	0.0005	0
ALAETSYVK	9	1				<0.0006	0.0002	0.17	0.39	0
VLGTLEEV	8	1		39	2.1	<0.0007	0.0088	0	0	0
SLQLVFGI	8	1		150	2.1	<0.0007	0.0094	0	0.0001	0
ILESLFRA	8	1		93	2.1	<0.0004	0.0017	0.0003	0	0.0001
FLLLKYRA	8	1		112	2.1	0.0036	0.0007	0.0003	0.0001	0

Sequence	AA	Mage Strain	Mol.	Pos.	Motif	A1	A2.1	A3.2	A11	A24
GLVCVQAA	8	1		24	2.1	0.0016	0.0008	0.0008	0	0
VLVTCLGL	8	1		170	2.1	<0.0007	0.0010	0.0001	0	0
KVADLVGFL	9	1		105	2.1	<0.0008	0.0091	0.0013	0.0005	0
YVLVTCLGL	9	1		169	2.1					
IMPKTGFLI	9	1		188	2.1	<0.0008	0.0035	0	0	3.2
GLLGDNQIM	9	1			A2.1	<0.0008	0.0054	0	0	0.0002
GLVCVQAAT	9	1		24	2.1	0.0030	0.0007	0.0026	0	0.0001
VADLVGFLL	9	1		106	2.1	0.032	0.0011	0.0054	0.0008	0.0007
YLEYGRCRTV	10	1		248	2.1	0.0008	0.0097	0.0001	0	0
SLQLVFGIDV	10	1		150	2.1	0.0028	0.0047	0.0013	0.0001	0.0001
IMPKTGFLII	10	1		188	2.1	<0.0008	0.0007	0	0	0.050
ALGLVCVQAA	10	1		22	A2.1	0.0011	0.0002	0.0003	0	0
EIWEELSVMEV	11	1		213	A2.1	0.0007	0.013	0.0001	0.0001	0
FLIIVLVMIAM	11	1			A2.1	0.023	0.0031	0.016	0.0014	0.0011
VIPHAMSSCGV	11	1		257	2.1	<0.0009	1.4	0	0	0
CILESCFRAVI	11	1			A2.1	0.079	0.0017	0.058	0.0005	0.0008
QIMPKTGFLII	11	1		187	2.1	<0.0009	0.0003	0	0	0.0030
GFLLLKYRA	9	1						0.0004	0.0002	
CFPEIFGKA	9	1						0	0	
FFFPSLREA	9	1						0	0	
FPPSLREAA	9	1						0	0	
RSLHCKPEEA	10	1						0.0001	0.0008	

Sequence	AA	Mage Strain	Mol.	Pos.	Motif	A1	A2.1	A3.2	A11	A24
EFLWGPRALA	10	1						0	0	
RFFFPSLREA	10	1						0.0004	0	
FFFPSLREAA	10	1						0	0	

Sequence	Antigen	Strain	Molecule	Position	Motif	A1 Binding	A2 Binding	A3 Binding	A11 Binding	A24 Binding	Max. Binding
ALFLGFLGAA	HIV	MN	gp160	518	A02		0.4950				0.4950
MLQLTVWGI	HIV	MN	gp160	566	A02		0.2450				0.2450
RVIEVLQRA	HIV	MN	gp160	829	A02		0.1963				0.1963
KLTPLCVTL	HIV	MN	gp160	120	A02		0.1600				0.1600
LLIAARIVEL	HIV	MN	gp160	776	A02		0.1550				0.1550
SLLNATDIAV	HIV	MN	gp160	814	A02		0.1050				0.1050
ALFLGFLGA	HIV	MN	gp160	518	A02		0.0945				0.0945
HMLQLTVWGI	HIV	MN	gp160	565	A02		0.0677				0.0677
LLNATDIAV	HIV	MN	gp160	815	A02		0.0607				0.0607
ALLYKLDIV	HIV	MN	gp160	179	A02		0.0362				0.0362
WLWYIKIFI	HIV	MN	gp160	679	A02		0.0355				0.0355
TIIVHLNESV	HIV	MN	gp160	288	A02		0.0350				0.0350
LLQYWSQEL	HIV	MN	gp160	800	A02		0.0265				0.0265
IMIVGGLVGL	HIV	MN	gp160	687	A02		0.0252				0.0252
LLYKLDIVSI	HIV	MN	gp160	180	A02		0.0245				0.0245
FLAIIWVDL	HIV	MN	gp160	753	A02		0.0233				0.0233
TLQCKIKQII	HIV	MN	gp160	415	A02		0.0200				0.0200
GLVGLRIVFA	HIV	MN	gp160	692	A02		0.0195				0.0195
FLGAAGSTM	HIV	MN	gp160	523	A02		0.0190				0.0190
IISLWDQSL	HIV	MN	gp160	107	A02		0.0179				0.0179
TVWGIKQLQA	HIV	MN	gp160	570	A02		0.0150				0.0150
LLGRRGWEV	HIV	MN	gp160	785	A02		0.0142				0.0142
AVLSIVNRV	HIV	MN	gp160	701	A02		0.0132				0.0132

Sequence	Antigen	Strain	Molecule	Position	Motif	A1 Binding	A2 Binding	A3 Binding	A11 Binding	A24 Binding	Max. Binding
FIMIVGGLV	HIV	MN	gp160	686	A02		0.0131				0.0131
LLNATDIAVA	HIV	MN	gp160	815	A02		0.0117				0.0117
FLYGALLLA	PLP	Human		80	A02		1.9000				1.9000
SLLTFMIAA	PLP	Human		253	A02		0.5300				0.5300
FMIAATYNFAV	PLP	Human		257	A02		0.4950				0.4950
RMYGVLPWI	PLP	Human		205	A02		0.1650				0.1650
IAATYNFAV	PLP	Human		259	A02		0.0540				0.0540
GLLECCARCLV	PLP	Human		2	A02		0.0515				0.0515
YALTVVWLL	PLP	Human		157	A02		0.0415				0.0415
ALTVVWLLV	PLP	Human		158	A02		0.0390				0.0390
FLYGALLL	PLP	Human		80	A02		0.0345				0.0345
SLCADARMYGV	PLP	Human		199	A02		0.0140				0.0140
LLVFACSAV	PLP	Human		164	A02		0.0107				0.0107

Table 10

AA	SEQUENCE	SOURCE
9	YIFATCLGL	MAGE 3 169
9	IMPKTGFLI	MAGE 1 188
10	IMPKTGFLII	MAGE 1 188
15	MLGSVVGNWQYFFPV	MAGE 3 POL 75
9	VMPKTGLLI	MAGE 2 188
9	IMPKAGLLI	MAGE 3 188
10	IMPKAGLLII	MAGE 3 188
9	RLWHYPCTV	HCV Env2 614
9	RLWHYPCTI	HCV Env2 614
9	FLLLADARI	HCV Env2
9	GVWPLLLLL	HCV Env2 792
9	GMWPLLLLL	HCV Env2 792
9	YLNTPGLPV	HCV NS3/NS4 1542
9	YMNTPGLPV	HCV NS3/NS4 1542
9	VILDSFDPL	HCV NS5 2251
9	ILMTHFFSI	HCV NS5 2843
9	ILMTHFFSV	HCV NS5 2843
9	LMAVVLASL	gp100 606
9	SLSLGFLFL	PAP 13
10	YMIMVKCWMI	c-ErbB2 952
10	GLHGQDLFGI	PAP 196
9	AILSVSSFL	P. falciparum CSP 6
9	GLIMVLSFL	P. falciparum CSP 425
9	VLLGGVGLV	P. falciparum EXP-1 91
9	GLLGNVSTV	P. falciparum EXP-1 83
9	LLGNVSTVL	P. falciparum EXP-1 84
9	VLAGLLGNV	P. falciparum EXP-1 80

AA	SEQUENCE	SOURCE
9	KILSVFFLA	P. falciparum EXP-1 2
9	FLIFFDLFL	P. falciparum TRAP 14
9	LIFFDLFLV	P. falciparum TRAP 15
9	FMKAVCVEV	P. falciparum TRAP 230
9	LLMDCSGSI	P. falciparum TRAP 51
10	ILSVSSFLFV	P. falciparum CSP 7
10	VLLGGVGLVL	P. falciparum EXP-1 91
10	GLLGNVSTVL	P. falciparum EXP-1 83
10	FLIFFDLFLV	P. falciparum TRAP 14
10	GLALLACAGL	P. falciparum TRAP 507
9	KIWEELSML	MAGE2 220
9	TLMSAMTNL	Prost.Ca PAP 112
9	LLLARAASL	Prost.Ca PAP 6
9	ALDVYNGLL	Prost.Ca PAP 299
9	VTWIGAAPL	PSA 8
10	ALIETSYVKV	MAGE2 277
10	SLSLGFLFLL	Prost.Ca PAP 13
10	RTLMSAMTNL	PAP 111
10	FLPSDFFPSV(CONH2)	HBc 18-27
10	FLPSDFFPSV-NH2	HBc 18-27
9	ILGFVFTLT-NH2	Flu Matrix 59-67
10	KGILGFVFTL-NH2	Flu Matrix 57-66
11	FLPSDFFPSVR	HBc 18-28
9	FLPSDFFPS	HBc 18-26
9	GILGKVFTL	Flu Matrix 58-66 analog
9	FLSKQYLNL	HBV polymerase
9	KLQCVPLHV	PSA 166-174 P/D

AA	SEQUENCE	SOURCE
9	KLQCVPLHV	PSA 166-174 P/D
9	KLQCVPLHV	PSA 166-174 P/D
9	KLYEIVAKV	A2.1 consensus
9	KLAEYVAKV	A2.1 consensus
9	KLAEIVYKV	A2.1 consensus
9	TLTSCNTSV	HIV gp 120 env. RE trans. 197
9	ALMEKIYQV	A2.1 consensus peptide
9	ALSEKIYQV	A2.1 consensus peptide
9	FLMSYFPSV	941.01 9-mer analog
9	FLPSYFPSV	941.01 9-mer analog
10	FLMSDYFPSV	941.01 M2 analog
9	FLYCYFALV	Chiron consensus
9	FMYCYFALV	Chiron consensus
10	SLVGFGILCV	Chiron consensus
10	SLMGCGLFWV	Chiron consensus
8	GLLGPLLV	HBVadr-ENV
9	AMAKAAAAI	A2.1 poly-A
10	MMWYWGPSLY	HBV
9	FLPSYFPSA	analog of 994.02: chiron comb
9	FAPSYFPSV	analog of 994.02: chiron comb
9	FLPSYFPSS	analog of 994.02: chiron comb
9	FSPSYFPSV	analog of 994.02: chiron comb
9	IMPKTGFLI	MAGE-1
9	VADLVGFLL	MAGE-1
11	EIWEELSVMEV	MAGE-1
11	FLIIVLVMIAM	MAGE-1
11	VIPHAMSSCGV	MAGE-1
11	CILESCFRAVI	MAGE-1
9	YIFATCLGL	MAGE3

AA	SEQUENCE	SOURCE
9	YIFATCLGL	MAGE3
11	KMVELVVHFLLL	MAGE2 112-122
11	HLFIYATCLGL	MAGE3 174-184
9	GLQDCTMLV	HCV NS5 2727-2735
8	TLGIVSPI	HPV, analog of 1088.01
8	TLGIVXPI	HPV, analog of 1088.01
10	FLLAQFTSAI	HBV POL 513
11	VLLDYQGMLPV	HBV env
11	CILLLCLIFLL	HBV env
9	FLGGSPVCL	HBV env
11	TVIEYLVSFGV	HBV core 114-124
11	TVLEYLVSFGV	HBV core 114-124
10	FLLAQFTSAI	HBV pol
9	GLYSSTVPI	HBV pol
9	GLYSSTAPI	HBV pol
9	GLDVLTAKV	HIV form VIN.
9	RILGAVAKV	HIV form VIN.
9	LLFGYPVYV	HTLV, tax 11-19
9	ALFGYPVYV	tax 11-19, SAAS
9	LLFGAPVYV	tax 11-19, SAAS
9	LLFGYAVYV	tax 11-19, SAAS
9	LLFGYPVAV	tax 11-19, SAAS
9	AAGIGILTV	MART1 27-35
9	GILTVILGV	MART1 31-39
9	ILTVILGVL	MART1 32-40
9	VILGVLLLI	MART1 35-43
9	ALMDKSLHV	MART1 56-64
10	TVILGVLLLI	MART1
10	LLDGTATLRL	MART1
10	ILSVSSFLFV	Plas. falcip. CSA-A 7-16
9	GLIMVLSFL	Plas. falcip. CSA-A 401-409

AA	SEQUENCE	SOURCE
9	IMVLSFLFL	Plas. falcip. CSA-A 403-411
10	FLIFFDLFLV	Plas. falcip. TRAP-A 14-23
9	FMKAVCVEV	Plas. falcip. TRAP-A 200-207
9	IMPGQEAGL	gp100
9	GLGQVPLIV	gp100
9	LMAVVLASL	gp100
9	RLMKQDFSV	gp100
9	HLAVIGALL	gp100
9	LLAVGATKV	gp100
9	MLGTHTMEV	gp100
10	LLDGTATLRL	gp100
10	VLYRYGSFSV	gp100
10	VLPSPACQLV	gp100
10	SLADTNSLAV	gp100
10	VLMAVVLASL	gp100
10	LMAVVLASLI	gp100
10	RLDCWRGGQV	gp100
10	AMLGTHTMEV	gp100
10	ALDGGNKHFL	gp100
9	YLEPGPVTA	gp100
10	LLNATAIAVA	
11	SLLNATAIAVA	
9	KTWGQYWQV	gp100
9	ITDQVPFSV	gp100
9	YLEPGPVTA	gp100
10	LLDGTATLRL	gp100
10	VLYRYGSFSV	gp100
10	ALDGGNKHFL	gp100
9	GILTVILGV	MART1 31-39
9	YMNGTMSQV	Human Tyrosinase
9	MLLAVLYBL	Human Tyrosinase
9	LLWSFQTSA	Human Tyrosinase

AA	SEQUENCE	SOURCE
9	YLTLAKHTI	Human Tyrosinase
9	FLPWHRLFL	Human Tyrosinase
9	FLLRWEQEI	Human Tyrosinase
9	RIWSWLLGA	Human Tyrosinase
9	LLGAAMVGA	Human Tyrosinase
9	AMVGAVLTA	Human Tyrosinase
9	VLTALLAGL	Human Tyrosinase
9	ALLAGLVSL	Human Tyrosinase
9	LLAGLVSLL	Human Tyrosinase
10	BLLWSFQTSA	Human Tyrosinase
10	WMHYYVSMDA	Human Tyrosinase
10	FLPWHRLFLL	Human Tyrosinase
10	WLLGAAMVGA	Human Tyrosinase
10	AMVGAVLTAL	Human Tyrosinase
10	VLTALLAGLV	Human Tyrosinase
10	TALLAGLVSL	Human Tyrosinase
10	ALLAGLVSLL	Human Tyrosinase
9	NLTDALLQV	P. falciparum SSP2 132
9	SAWENVKNV	P. falciparum SSP2 218
10	FLIFFDLFLV	P. falciparum SSP2 14
9	NLNDNAIHL	P. falciparum SSP2 80
10	YLLMDCSGSI	P. falciparum SSP2 51
9	TLQDVSLEV	controls

Table 11

AA	SEQUENCE	SOURCE
9	ALYWFRTGI	HPV 6b/11 E1 319
	LLDGNPMSI	HPV 6b/11 E1 540
9	NAWGMVLLV	HPV 6b/11 E1 270
9	SLYAHIQWL	HPV 6b/11 E1 260
9	TLIKCPPLL	HPV 6b/11 E1 556
9	GIYDALFDI	PSMAg 707
9	YLSGANLNL	CEA 605
9	VLYGPDTPI	CEA 589
9	IMIGVLVGV	CEA 691
9	LLTFWNPPT	CEA 24
9	KLTEMVQWA	HPV 6b/11 E1 357
9	YMDTYMRNL	HPV 6b/11 E1 532
10	NLLDGNPMSI	HPV 6b/11 E1 539
10	SLYAHIQWLT	HPV 6b/11 E1 260
10	TLIKCPPLLV	HPV 6b/11 E1 556
10	MVFELANSIV	PSMAg 583
10	YLWWVNNQSL	CEA 176
10	YLWWVNNQSL	CEA 354
10	YLWWVNGQSL	CEA 532
10	GIMIGVLVGV	CEA 690
10	VLYGPDAPTI	CEA 233
10	KLIEPLSLYA	HPV 6b/11 E1 254
10	WLCAGALVLA	PSMAg 20
10	IMIGVLVGVA	CEA 691

AA	SEQUENCE	SOURCE
9	YLYQLSPPI	HTLV-I tax 155
9	LLFEEYTNI	HTLV-I tax 307
9	QLGAFLTNV	HTLV-I tax 178
9	TLTAWQNGL	HTLV-I tax 226
9	ALQFLIPRL	HTLV-I tax 67
9	TLGQHLPTL	HTLV-I tax 123
9	FAFKDLFVV	HPV 18 E6 47
9	RLLQLLFRA	GCDFP-15 2
9	CMVVKTYLI	GCDFP-15 65
9	LLLVLCLQL	GCDFP-15 15
9	ILYAHIQCL	HPV18 E1 266
9	SLACSWGMV	HPV16 E1 266
9	CLYLHIQSL	HPV16 E1 259
9	YLVSPLSDI	HPV16 E1 90
9	VMFLRYQGV	HPV16 E1 443
9	KLLSKLLCV	HPV16 E1 292
9	ALDGNPISI	HPV18 E1 546
9	AVFKDTYGL	HPV18 E1 216
9	LLTTNIHPA	HPV18 E1 570
9	LLQQYCLYL	HPV16 E1 254

AA	SEQUENCE	SOURCE
9	AMLAKFKEL	HPV16 E1 206
9	ALDGNLVSM	HPV16 E1 539
9	FLGALKSFL	HPV18 E1 463
9	FIHFIQGAV	HPV18 E1 497
10	TLLLVLCLQL	GCDFP-15 14
10	LLFRASPATL	GCDFP-15 6
10	SLMKFLQGSV	HPV16 E1 489
10	SLACSWGMVV	HPV16 E1 266
10	FLQGSVICFV	HPV16 E1 493
10	FIQGAVISFV	HPV18 E1 500
10	KLLCVSPMCM	HPV16 E1 296
10	FILYAHIQCL	HPV18 E1 265
10	FVNSTSHFWL	HPV18 E1 508
10	ILLTTNIHPA	HPV18 E1 569
10	TLLQQYCLYL	HPV16 E1 253
9	GLLGWSPQA	HBV ENV 62
9	GLACHQLCA	HER2/neu
9	ILDEAYVMA	HER2/neu
9	SIISAVVGI	HER2/neu
9	VVLGVVFGI	HER2/neu
9	YMIMVKCWM	HER2/neu
10	ALCRWGLLLA	HER2/neu
10	QLFEDNYALA	HER2/neu

AA	SEQUENCE	SOURCE
9	HMWNFISGI	HCV consensus
9	VIYQYMDDL	HIV POL 358
9	SLYNTVATL	HIV GAG 77
10	TVWGIKQLQA	HIV ENV 735
9	LLLEAGALV	MSH 99
9	VLETAVGLL	MSH 92
9	CLALSDLLV	MSH 79
9	FLSLGLVSL	MSH 45
9	SLVENALVV	MSH 52
9	AIIDPLIYA	MSH 291
9	FLCWGPFFL	MSH 251
9	FLALIICNA	MSH 283
9	TILLGIFFL	MSH 244
9	RLLGSLNST	MSH 9
9	SLYNTVATL	HIV p17/5B 77-8
9	VIYQYMDDL	HIV RT/50A 346-
9	ILKEPVHGV	HIV RT/IV9 476-

Table 12

PEPTIDE NO.	PEPTIDE LENGTH	SEQUENCE
1237.01	9	FLWGPQALV
1237.02	9	FLWGPNALV
1237.03	9	FLWGPHALV
1237.04	9	FLWGPKALV
1237.05	9	FLWGPFALV
26.0158	9	AVIGALLAV
26.0172	9	LLHLAVIGA
26.0186	9	SLADTNSLA
26.0192	9	VMGTTLAEM
26.0240	9	LLAVLYCLL
26.0383	10	FLRNQPLTFA
26.0390	10	HLAVIGALLA
26.0395	10	LAVIGALLAV
26.0418	10	TLAEMSTPEA
26.0423	10	YLAEADLSYT
26.0497	10	MLLAVLYCLL
1183.10	10	VLYRYGSFSV
27.0007	9	ILSSLGLPV
27.0012	9	LLFLGVVFL
27.0019	9	GLYGAQYDV
27.0022	9	FVVALIPLV
27.0023	9	GLMTAVYLV
27.0027	9	ALVLLMLPV
27.0028	9	ILLSIARVV
27.0029	9	SLYFGGICV
27.0030	9	QLIPCMDVV
27.0031	9	VLQQSTYQL
27.0032	9	AIHNVVHAI
27.0034	9	GLHGVGVSV
27.0035	9	GLVDFVKHI
27.0036	9	LLFRFMRPL
27.0038	9	LMLPGMNGI
27.0043	9	TVLRFVPPL
27.0044	9	MLGNAPSVV
27.0050	9	YLDLALMSV
27.0064	9	RMPEAAPPV

PEPTIDE NO.	PEPTIDE LENGTH	SEQUENCE
27.0082	9	FLLPDAQSI
27.0083	9	MTYAAPLFV
27.0088	9	LLPLGYPFV
27.0089	9	GLYYLTTEV
27.0090	9	MALLRLPLV
27.0091	9	RLPLVLPAV
27.0093	9	RMFAANLGV
27.0095	9	RLLDDTPEV
27.0096	9	YLYVHSPAL
27.0100	9	GLYLSQIAV
27.0101	9	YLSQIAVLL
27.0102	9	SLAGFVRML
27.0137	10	ATYDKGILTV
27.0146	10	KIFMLVTAVV
27.0151	10	FLLADERVRV
27.0153	10	MLATDLSLRV
27.0154	10	RLQPQVGWEV
27.0161	10	FLMPVEDVFI
27.0165	10	RMSRVTTFTV
27.0168	10	LALVLLMLPV
27.0169	10	ALVLLMLPVV
27.0170	10	GIVSGILLSI
27.0171	10	SLYFGGICVI
27.0173	10	QLIPCMDVVL
27.0181	10	LLFRFMRPLI
27.0183	10	VLLEDGGVEV
27.0184	10	AMPAYNWMTV
27.0186	10	GLAGTVLRFV
27.0188	10	VLIAFGRFPI
27.0189	10	FLTCDANLAV
27.0197	10	AIAWGAWGEV
27.0204	10	LLLETSWEAI
27.0217	10	RMPEAAPPVA
27.0223	10	WMAETTLGRV
27.0226	10	AMALLRLPLV
27.0229	10	FMSLAGFVRM
27.0266	11	SLLTEVETYVL

PEPTIDE NO.	PEPTIDE LENGTH	SEQUENCE
27.0268	11	GILGFVFTLTV
27.0269	11	VLDVGDAYFSV
27.0271	11	KIWEELSMLEV
27.0272	11	STLVEVTLGEV
27.0273	11	GLAPPQHLIRV
27.0274	11	HLIRVEGNLRV
27.0005	9	YLLALRYLA
27.0013	9	GLYRQWALA
27.0017	9	LLWQDPVPA
27.0040	9	ALLSDWLPA
27.0045	9	WLLIDTSNA
27.0046	9	MLASTLTDA
27.0081	9	YLSEGDMAA
27.0094	9	LLACAVIHA
27.0144	10	LLCCSGVATA
27.0191	10	LLATVFKLTA
27.0192	10	KLTADGVLTA
27.0195	10	GLGGLGLFFA
28.0064	8	TLGIVXPI
28.0065	8	ALGTTXYA
28.0293	9	FLLTRILTV
28.0294	9	ALMPLYACV
28.0295	9	LLAQFTSAV
28.0296	9	LLPFVQWFV
28.0297	9	FLLAQFTSV
28.0298	9	KLHLYSHPV
28.0299	9	KLFLYSHPI
28.0300	9	LLSSNLSWV
28.0301	9	FLLSLGIHV
28.0302	9	MMWYWGPSV
28.0303	9	VLQAGFFLV
28.0304	9	PLLPIFFCV
28.0305	9	FLLPIFFCL
28.0306	9	VLLDYQGMV
28.0307	9	YMDDVVLGV
28.0308	9	YMFDVVLGA
28.0309	9	GLLGWSPQV

PEPTIDE NO.	PEPTIDE LENGTH	SEQUENCE
28.0342	9	YMIMVKXWM
28.0343	9	YIFATXLGL
28.0345	9	SLHXKPEEA
28.0346	9	ALGLVXVQA
28.0348	9	LLMDXSGSI
28.0349	9	FAFRDLXIV
28.0352	9	GTLGIVXPI
28.0353	9	TLGIVXPIX
28.0354	9	LLWFHISXL
28.0355	9	KLTPLXVTL
28.0356	9	ALVEIXTEM
28.0357	9	LTFGWXFKL
28.0359	9	KLQXVDLHV
28.0360	9	FMKAVXVEV
28.0361	9	LLQQYXLYL
28.0362	9	XLYLHIQSL
28.0363	9	SLAXSWGMV
28.0364	9	ILYAHIQXL
28.0365	9	KLLSKLLXV
28.0366	9	PLLPIFFXL
28.0367	9	TLIKXPPLL
28.0368	9	ALMPLYAXI
28.0370	9	XILESLFRA
28.0609	10	FLLAQFTSAV
28.0610	10	YLHTLWKAGV
28.0611	10	YLFTLWKAGI
28.0612	10	YLLTLWKAGI
28.0613	10	LLFYQGMLPV
28.0614	10	LLLYQGMLPV
28.0615	10	LLVLQAGFFV
28.0616	10	ILLLCLIFLV
28.0650	10	ALXRWGLLL
28.0651	10	KLPDLXTEL
28.0652	10	HLYQGXQVV
28.0653	10	XILESLFRA
28.0654	10	KLQXVDLHV
28.0655	10	YIFATXLGL

PEPTIDE NO.	PEPTIDE LENGTH	SEQUENCE
F111.01	9	SLYNTVATL
F111.02	9	ALYNTVATL
F111.04	9	SLANTVATL
F111.06	9	SLFNAVATL
F111.07	9	SLFNLLATL
F111.10	9	SLFNTIAVL
F111.11	9	SLFNAVAVL
F111.09	9	SLFNTIVVL
F111.12	9	SLFNAIAVL
F111.13	9	SLFNTVAVL
F111.14	9	SLFNTVCVI
F111.15	9	SLHNTVATL
F111.17	9	SLHNTVAVL
F111.18	9	SLYATVATL
F111.19	9	SLYNAVATL
F111.21	9	SLYNTAATL
F111.22	9	SLYNTIAVL
F111.23	9	SLYNTSATL
F111.25	9	SLYNTVAVL
F111.26	9	SLYNTVATA
F111.27	9	SLYNAIATL
F111.28	9	SLYNLVAVL
F111.29	9	SLFNLLAVL
F111.32	9	SLFNTVVTL
F111.34	9	SLYNTVAAL
1039.031	9	MMWYWGPSL
1211.40	10	SLLNATAIAV
	10	TIHDIILECV
	9	FAFRDLCIV
	9	GTLGIVCPI
	9	TLGIVCPIC

Table 13

AA	SEQUENCE	SOURCE
9	IPQSLDSWW	HBV ENV 191
9	IPIPSSWAF	HBV ENV 313
9	TPARVTGGV	HBV POL 365
9	LPIFFCLWV	HBV ENV 379
9	HPAAMPHLL	HBV POL 440
9	FPHCLAFSY	HBV POL 541
9	DPSRGRLGL	HBV POL 789
9	QPRGRRQPI	HCV Core 57
9	SPRGSRPSW	HCV Core 99
9	DPRRRSRNL	HCV Core 111
9	LPGCSFSIF	HCV Core 168
9	YPCTVNFTI	HCV E2 622
9	LPALSTGLI	HCV E2 681
9	HPNIEEVAL	HCV NS3 1358
9	SPGALVVGV	HCV NS4 1887

AA	SEQUENCE	SOURCE
9	SPGQRVEFL	HCV NS5 2615
9	APTLWARMI	HCV NS5 2835
9	FPRIWLHJL	HIV VPR 34
9	SPTRRELQV	HIV POL 37
9	FPVRPQVPL	HIV NEF 84
9	RPQVPLRPM	HIV NEF 87
9	KPCVKLTPL	HIV ENV 123
9	SPRTLNAWV	HIV GAG 153
9	FPISPIETV	HIV POL 171
9	SPAIFQSSM	HIV POL 327
9	NPDIVIYQY	HIV POL 346
9	GPGHKARVL	HIV GAG 360
9	LPEKDSWTV	HIV POL 417
9	YPLASLRSL	HIV GAG 507
9	VPRRKAKII	HIV POL 991
9	TPTLHEYML	HPV16 E7 5
9	KPLNPAEKL	HPV18 E6 110
9	NPAEKLRHL	HPV18 E6 113
9	VPISHLYIL	MAGE2 170
9	MPKTGLLII	MAGE2 196

A A	SEQUENCE	SOURCE
9	DPACYEFLW	MAGE2 265
9	EPHISYPPL	MAGE2 296
9	YPPLHERAL	MAGE2 301
9	LPTTMNYPL	MAGE3 71
9	DPIGHLYIF	MAGE3 170
9	MPKAGLLII	MAGE3 196
9	GPHISYPPL	MAGE3 296
9	HPSDGKCNL	P. falciparum S
9	RPRGDNFAV	P. falciparum S
9	QPRPRGDNF	P. falciparum S
9	LPNDKSDRY	P. falciparum S
10	LPLDKGIKPY	HBV POL 123
10	TPARVTGGVF	HBV POL 365
10	FPHCLAFSYM	HBV POL 541
10	LPRRGPRLGV	HCV Core 37
10	APLGGAARAL	HCV Core 142
10	LPGCSFSIFL	HCV Core 168
10	VPASQVCGPV	HCV E2 497
10	YPCTVNFTIF	HCV E2 622

AA	SEQUENCE	SOURCE
10	SPLLLSTTEW	HCV E2 663
10	RPSGMFDSSV	HCV NS3 1506
10	LPVCQDHLEF	HCV NS3 1547
10	KPTLHGPTPL	HCV NS3 1614
10	TPLLYRLGAV	HCV NS3 1621
10	NPAIASLMAF	HCV NS4 1783
10	LPAILSPGAL	HCV NS4 1882
10	SPGALVVGVV	HCV NS4 1887
10	APTLWARMIL	HCV NS5 2835
10	IPVGEIYKRW	HIV GAG 261
10	YPLASLRSLF	HIV GAG 507
10	APTKAKRRVV	HIV ENV 547
10	VPISHLYILV	MAGE2 170
10	MPKTGLLIIV	MAGE2 196
10	HPRKLLMQDL	MAGE2 241
10	LPTTMNYPLW	MAGE3 71
10	MPKAGLLIIV	MAGE3 196

AA	SEQUENCE	SOURCE
10	IPYSPLSPKV	P. falciparum S
10	TPYAGEPAPF	P. falciparum S
9	FPDHQLDPA	HBV ENV 14
9	YPALMPLYA	HBV POL 640
9	LPVCAFSSA	HBV X 58
9	APLGGAARA	HCV 142
9	DPTTPLARA	HCV 2806
9	FPYLVAYQA	HCV 1582
9	LPAILSPGA	HCV 1882
9	NPAIASLMA	HCV 1783
9	TPIDTTIMA	HCV 2551
9	TPLLYRLGA	HCV 1621
9	WPLLLLLLA	HCV 793
9	NPYNTPVFA	HIV POL 225
9	APLLLARAA	PAP 4
9	HPQWVLTAA	PSA 52
10	IPIPSSWAFA	HBV ENV 313
10	TPPAYRPPNA	HBV NUC 128
10	APFTQCGYPA	HBV POL 633
10	LPIHTAELLA	HBV POL 712
10	GPCALRFTSA	HBV X 67

A A	SEQUENCE	SOURCE
10	DPTTPLARAA	HCV 2806
10	IPQAVVDMVA	HCV 339
10	LPCSFTTLPA	HCV 674
10	QPEKGGRKPA	HCV 2567
10	VPHPNIEEVA	HCV 1356
10	IPAETGQETA	HIV POL 820
10	LPQGWKGSPA	HIV POL 320
10	FPDLESEFQA	MAGE2/3 98
10	DPIGHLYIFA	MAGE3 170
9	EPLSLYAHI	HPV 6b/11 E1 2
9	PPLLVTSNI	HPV 6b/11 E1 5
9	SPRLDAIKL	HPV 6b/11 E1 1
9	TPKKNCIAI	HPV 6b/11 E1 4
9	FPFDRNGNA	HPV 6b/11 E1 5
10	CPPLLVTSNI	HPV 6b/11 E1 5
10	FPFDRNGNAV	HPV 6b/11 E1 5
8	GPLLVLQA	HBV ENV 173
8	IPIPSSWA	HBV ENV 313

AA	SEQUENCE	SOURCE
8	VPFVQWFV	HBV ENV 340
8	LPIFFCLW	HBV ENV 379
8	RPPNAPIL	HBV NUC 133
8	MPLSYQHF	HBV POL 1
8	HPAAMPHL	HBV POL 429
8	SPFLLAQF	HBV POL 511
8	YPALMPLY	HBV POL 640
8	SPTYKAFL	HBV POL 659
8	VPSALNPA	HBV POL 769
8	HPvhAGPI	HIV con. GAG
8	GPGvRyPL	HIV con. NEF
8	SPIETVPV	HIV con. POL
8	NPYNTPVF	HIV con. POL
8	LPIQKETW	HIV con. POL

A A	SEQUENCE	SOURCE
8	VPRRKaKi	HIV con. POL
8	VpLQLPPI	HIV con. REV
8	VPLAMKLI	P. falciparum
8	LPYGRTNL	P. falciparum
8	RPRGDNFA	P. falciparum
8	IPQQEPNI	P. falciparum
8	TPFAGEPA	P. falciparum
9	SPINTIAEA	HPV 6b E1 93
9	SPISNVANA	HPV 11 E1 93
9	SPRLDAIKL	HPV 6b/11 E1 1
9	EPLSLYAHI	HPV 6b/11 E1 2
9	EPPKIQSGV	HPV 6b/11 E1 3
9	IPFLTKFKL	HPV 6b E1 455
9	TPKKNCIAI	HPV 6b/11 E1 4
9	QPLTDAKVA	HPV 11 E1 512
9	PPLLVTSNI	HPV 6b/11 E1 5

A A	SEQUENCE	SOURCE
9	FPFDRNGNA	HPV 6b/11 E1 5
9	APLILSRIV	PSA 14
9	HPEDTGQVF	PSA 78
9	HPLYDMSLL	PSA 94
9	HPQKVTKFM	PSA 184
9	GPLVCNGVL	PSA 211
9	RPSLYTKVV	PSA 235
9	FPPEGVSIW	PAP 124
9	NPILLWQPI	PAP 133
9	LPFRNCPRF	PAP 156
9	IPSYKKLIM	PAP 277
9	LPPYASCHL	PAP 307
9	SPSCPLERF	PAP 348
9	CPLERFAEL	PAP 351
9	GPTLIGANA	gp100 74
9	LPDGQVIWV	gp100 97
9	VPLAHSSSA	gp100 198
9	QPLTFALQL	gp100 236
9	DPSGYLAEA	gp100 246
9	EPGPVTAQV	gp100 282
9	MPTAESTGM	gp100 366
9	TPAEVSIVV	gp100 401
9	LPKEACMEI	gp100 520
9	LPSPACQLV	gp100 545
9	VPLIVGILL	gp100 596
9	LPHSSSHWL	gp100 630

AA	SEQUENCE	SOURCE
9	CPIGENSPL	gp100 647
9	SPLLSGQQV	gp100 653
9	MPREDAHFI	MART1 1
9	APLGPQFPF	Tyrosinase 6
9	IPIGTYGQM	Tyrosinase 1
9	TPMFNDINI	Tyrosinase 1
9	LPWHRLFLL	Tyrosinase 2
9	IPYWDWRDA	Tyrosinase 2
9	SPASFFSSW	Tyrosinase 2
9	LPSSADVEF	Tyrosinase 3
9	SPLTGIADA	Tyrosinase 3
9	DPIFLLHHA	Tyrosinase 3
9	IPLYRNGDF	Tyrosinase 4
9	YPELPKPSI	CEA 141
9	LPVSPRLQL	CEA 185
9	LPVSPRLQL	CEA 363
9	NPPAQYSWL	CEA 442
9	LPVSPRLQL	CEA 541
9	IPQQHTQVL	CEA 632
9	NPPAQYSWF	CEA 264
9	LPSIPVHPI	Prost.Ca PSM
9	IPVHPIGYY	Prost.Ca PSM
9	RPFYRHVIY	Prost.Ca PSM
9	TPKHNMKAF	Prost.Ca PSM
9	FPGIYDALF	Prost.Ca PSM
9	RPRWLCAGA	Prost.Ca PSM
9	DPLTPGYPA	Prost.Ca PSM

AA	SEQUENCE	SOURCE
9	RPRRTILFA	Prost.Ca PSM
9	LPFDCRDYA	Prost.Ca PSM
9	LPIHTAELL	HBV POL 712
10	GPDAPTISPL	CEA 236
10	IPQQHTQVLF	CEA 632
10	QPIPVHTVPL	Prost.Ca PAP
10	HPYKDFIATL	Prost.Ca PAP
10	LPGCSPSCPL	Prost.Ca PAP
10	LPSWATEDTM	Prost.Ca PAP
10	VPLSEDQLLY	Prost.Ca PAP
10	FPHPLYDMSL	Prost.Ca PSA
10	RPGDDSSHDL	Prost.Ca PSA
10	HPQKVTKFML	Prost.Ca PSA
10	LPFDCRDYAV	Prost.Ca PSM
10	YPNKTHPNYI	Prost.Ca PSM
10	SPEFSGMPRI	Prost.Ca PSM
10	RPRWLCAGAL	Prost.Ca PSM
10	TPKHNMKAFL	Prost.Ca PSM
10	RPFYRHVIYA	Prost.Ca PSM
10	HPAAMPHLLV	HBV POL 429
9	SPREGPLPA	HER2/neu 1151
9	KPDLSYMPI	HER2/neu 605
9	HPPPAFSPA	HER2/neu 1208

AA	SEQUENCE	SOURCE
9	GPLPAARPA	HER2/neu 1155
9	APQPHPPPA	HER2/neu 1204
9	EPLTPSGAM	HER2/neu 698
9	LPTHDPSPL	HER2/neu 1101
9	DPLNNTTPV	HER2/neu 121
9	SPLTSIISA	HER2/neu 649
9	SPKANKEIL	HER2/neu 760
9	LPTNASLSF	HER2/neu 65
9	CPSGVKPDL	HER2/neu 600
9	SPLAPSEGA	HER2/neu 1073
9	MPNQAQMRI	HER2/neu 706
9	LPAARPAGA	HER2/neu 1157
9	LPQPPICTI	HER2/neu 941
9	SPAFDNLYY	HER2/neu 1214

AA	SEQUENCE	SOURCE
9	TPTAENPEY	HER2/neu 1240
9	LPSETDGYV	HER2/neu 1120
10	LPTNASLSFL	HER2/neu 65
10	CPAEQRASPL	HER2/neu 642
10	KPCARVCYGL	HER2/neu 336
10	APQPHPPPAF	HER2/neu 1204
10	SPGGLRELQL	HER2/neu 133
10	SPLTSIISAV	HER2/neu 649
10	MPNQAQMRIL	HER2/neu 706
10	SPYVSRLLGI	HER2/neu 779
10	HPPPAFSPAF	HER2/neu 1208
10	SPREGPLPAA	HER2/neu 1151
10	NPHQALLHTA	HER2/neu 488
10	MPYGCLLDHV	HER2/neu 801

AA	SEQUENCE	SOURCE
10	GPASPLDSTF	HER2/neu 995
9	LPTTLFQPV	HTLV-I tax 21
9	IPPSFLQAM	HTLV-I tax 10
9	FPGFGQSLL	HTLV-I tax 4
9	WPLLPHVIF	HTLV-I tax 16
9	SPPITWPLL	HTLV-I tax 16
9	VPYKRIEEL	HTLV-I tax 18
9	RPQNLYTLW	HTLV-I tax 13
9	CPKDGQPSL	HTLV-I tax 26
9	RPNDEVTAV	GCDFP-15 47
9	SPATLLLVL	GCDFP-15 11
9	WPYLHNRLV	HPV16 E1 576
9	QPFILYAHI	HPV18 E1 263
9	SPRLKAICI	HPV16 E1 107

AA	SEQUENCE	SOURCE
9	SPLGERLEV	HPV18 E1 97
9	SPRLQEISL	HPV18 E1 110
9	RPIVQFLRY	HPV18 E1 447
10	WPYLHNRLVV	HPV16 E1 576
10	WPYLESRITV	HPV18 E1 583
10	QPPKLRSSVA	HPV18 E1 315
10	EPPKLRSTAA	HPV16 E1 308
9	DPSRGRLGL	HBV POL 778
9	HPAAMPHLL	HBV POL 429
9	IPIPSSWAF	HBV ENV 313
10	TPARVTGGVF	HBV POL 354
10	FPHCLAFSYM	HBV POL 530
9	LPVCAFSSA	HBV X 58
9	YPALMPLYA	HBV POL 640
9	APLLLARAA	PAP 4

A A	SEQUENCE	SOURCE
9	HPQWVLTAA	PSA 52
9	HPSDGKCNL	Pf SSP2 206
9	RPRGDNFAV	Pf SSP2 305
9	QPRPRGDNF	Pf SSP2 303
10	TPYAGEPAPF	Pf SSP2 539
9	GPHISYPPL	MAGE3 296
9	YPPLHERAL	MAGE2 301
9	VPISHLYIL	MAGE2 170
9	EPHISYPPL	MAGE2 296
9	LPTTMNYPL	MAGE3 71
9	MPKAGLLII	MAGE3 196
10	HPRKLLMQDL	MAGE2 241

Table 14

PEPTIDE	AA	SEQUENCE
25.0129	9	LPPLERLTL
26.0445	10	EPGPVTAQVV
26.0448	10	LPRIFCSCPI
26.0449	10	LPSPACQLVL
26.0455	10	VPLAHSSSAF
26.0458	10	VPRNQDWLGV
26.0476	10	APPAYEKLSA
26.0478	10	MPREDAHFIY
26.0519	10	APAFLPWHRL
26.0522	10	GPNCTERRLL
26.0523	10	IPLYRNGDFF
26.0529	10	TPRLPSSADV
19.0101	9	TPAEVSIVV
26.0554	11	APFTQCGYPAL
26.0561	11	NPADDPSRGRL
26.0564	11	RPPNAPILSTL
26.0566	11	SPFLLAQFTSA
26.0567	11	SPHHTALRQAI
26.0568	11	TPARVTGGVFL

WHAT IS CLAIMED IS:

1. A composition comprising an immunogenic peptide having an HLA binding motif, which immunogenic peptide is a peptide shown in Tables 3-14 or a peptide comprising a conservative substitution of a residue in a peptide shown in Table 3-14.

2. The composition of claim 1, wherein the immunogenic peptide is linked to a second oligopeptide.

3. The composition of claim 2, wherein the second oligopeptide is a peptide that induces a helper T response.

4. A composition comprising a nucleic acid molecule encoding an immunogenic peptide as shown in Tables 3-14, or a peptide comprising a conservative substitution of a residue of a peptide shown in Table 3-14.

5. The composition of claim 4, wherein the nucleic acid further comprises a sequence encoding a second immunogenic peptide.

6. The composition of claim 4, wherein the nucleic acid further comprises a sequence encoding an oligopeptide that induces a helper T response.

7. A method of inducing a cytotoxic T cell response comprising contacting a cytotoxic T cell with a peptide of claim 1.

INTERNATIONAL SEARCH REPORT	International application No. PCT/US98/05039

A. CLASSIFICATION OF SUBJECT MATTER
IPC(6) :A61K 39/00, 39/29; C07K 7/00, 14/02, 14/82
US CL : 424/185.1; 530/300, 328, 350
According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED
Minimum documentation searched (classification system followed by classification symbols)
U.S. : 424/185.1; 530/300, 328, 350

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched
STN file=reg of first sequence in Table 3. Examiner's MHC/peptide files.

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
STN file=reg sequence search of first sequence in Table 3. STN file=ca of hits on sequence search.

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
T	BRUSS, V. A short linear sequence in the pre-S domain of the large hepatitis B virus envelope protein required from virion formation. J. Virology. December 1997, Vol. 71, No. 12, pages 9350-9357. See entire document	1-3 and 7
Y	PREISLER-ADAMS, S. et al. Complete nucleotide sequence of a hepatitis B virus, subtype adw2, and identification of three types of C open reading frame. Nucleic Acids Res. 1993, Vol. 21, No. 9, page 2258. See entire document.	1-3 and 7
Y	RAMMENSEE, H. et al. Peptides naturally presented by MHC Class I molecules. Annu. Rev. Immunol. 1993, Vol. 11, pages 213-243, see entire article.	1-3 and 7

[X] Further documents are listed in the continuation of Box C. [ ] See patent family annex.

* Special categories of cited documents:
"A" document defining the general state of the art which is not considered to be of particular relevance
"E" earlier document published on or after the international filing date
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
"O" document referring to an oral disclosure, use, exhibition or other means
"P" document published prior to the international filing date but later than the priority date claimed
"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
12 MAY 1998	17 JUL 1998

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INTERNATIONAL SEARCH REPORT

International application No.
PCT/US98/05039

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	ENGELHARD, V. et al. Structure of peptides associated with MHC Class I molecules. Curr. Opin. Immunol. 1994, Vol. 6, pages 13-23, see entire document.	1-3 and 7

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US98/05039

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

See attached sheet.

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:
1-3 and 7

Remark on Protest
☐ The additional search fees were accompanied by the applicant's protest.
☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US98/05039

Observations where unity of invention is lacking (Continuation of item 2 of first sheet)
1. This International Search Authority has found 3453 inventions claimed in the International Application covered by the claims indicated below:

This application contains the following inventions or groups of inventions which are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for all inventions to be searched, the appropriate additional search fees must be paid.

Group I, claim(s) 1-3 and 7, drawn to compositions comprising peptides and methods of inducing CTL responses using such compositions. A review of Tables 3-14 indicates there are 2764 structurally different peptides recited.

Group II, claim(s) 4-6, drawn to nucleic acids encoding peptides. Claims 4-6 recite nucleic acids encoding the 2764 different peptides of Tables 3-14.

This application contains claims directed to more than one species of the generic invention. These species are deemed to lack Unity of Invention because they are not so linked as to form a single inventive concept under PCT Rule 13.1. The species are as follows:

Each of the 2764 different peptides recited by Tables 3-14 and each of the 2764 different nucleic acid sequences encoding the peptides of Tables 3-14. 2764 + 2764 = 5,528 total species.

The claims are deemed to correspond to the species listed above in the following manner:

The following claims are generic: claims 1-7 because they encompass all of the peptides or nucleic acid sequences encoding the peptides of Tables 3-14.

The first peptide species recited in Table 3 (FTF. . .LSK) will be examined. Each additional peptide species requires the payment of a separate fee. To have all the recited peptide species searched requires the payment of 2763 additional fees.

Upon payment for Group II, the Office will examine the first ten (or ten that the Applicant selects) nucleic acid species at no additional cost. Each four species of nucleic acids thereafter requires the payment of a separate fee. To have all the nucleic acid species searched requires the payment of (2764-10)/4 = 689 additional fees.

and it considers that the International Application does not comply with the requirements of unity of invention (Rules 13.1, 13.2 and 13.3) for the reasons indicated below:

The inventions listed as Groups I and II do not relate to a single inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: the peptides of Group I lack the corresponding technical structural and functional features of the nucleic acids of Group II.

The species listed above do not relate to a single inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, the species lack the same or corresponding special technical features for the following reasons: the 5528 different species of peptides recited by Tables 3-14 (or the nucleic acid sequences encoding such peptides) lack the same or corresponding special technical features of common structure and function, source of isolation and amino acid or nucleic acid identity. Each separate species would require a separate prior art search.